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REFERENCE	1 (bases 1 to 1161)				
AUTHORS	Chandrashekar, R. and Morales, T.H.				
TITLE	Parasitic helminth cuticlin nucleic acid molecules and uses thereof	olecules a	and 1	ses	thereof
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S Chandrashekar, R. and Morales, T.H.
Parasitic helminth cuticlin nucleic ac
Patent: US 6368600-A 2 09-APR-2002;
Location/Qualifiers
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                                      Submitted (15-JUL-1999) Infectious Diseases, School of Medicine, 216 S. Kings Highway, St. Sequence update by submitter On Aug 1, 2000 this sequence version replaced Location/Qualifiers
                                                                                 Diseases, Ain Shams University, Abassia Squa
3 (bases 1 to 1380)
Curtis,K., Ramzy,R., Helmy,H., Adely,M. and
Direct Submission
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ATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTTCGTTTAAA 1140
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Ramzy,R., Helmy,H., Adely,M., Curtis,K. and Direct Submission Submitted (03-FEB-1999) Research & Training
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/organism="Wuchereria /db\_xref="taxon:6293" /dev\_stage="L3 larvae"

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SFHPLFVTKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFATQIVPMPVCRYEILDGG
PSGQPVQFATIGQPVYIKWTCDSETVDTFCAVVHSCFVDBGNGDKVELLNADGCALDK
FLLNNLEYPTDLMAGQEAHVYKKADRSQLFYQCJGITIKEPNSEGCRPQCTEPQGFG
AIKTRNGVYAAALRQAAAFRVLKKRDVRDENIVDVRTDLMALDINEECTSLPNALAHRS
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Pred. No. 3.8e-141;
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                                                                                     GGATGAATGTCGTTCAGATAGTAATGGACGGCAGGTAGCTGGAATCGAATTGGCAATGGA
                                                                                                  AGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGA
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Chandrashekar,R. and Morales,T.H.
Parasitic helminth cuticlin nucleic
Patent: US 6368600-A 6 09-APR-2002;
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AR204522
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patent US 6368600
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Pred. No. 9e-108;
0; Mismatches 193;
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                                                   ATTATCATTATTCTCCTTGTTATTCCTACTTTCTACTTGACCTACGTATCATCGATCCC
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                                                                 ATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTG-CATTGTCTTATTCGATTCC
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                                                                               tch 43.4%; al Similarity 76.9%; 652; Conservative
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Sequence
AR204523
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Chandrashekar,R. and Morales,T.H.
Parasitic helminth cuttolin nucleic
Patent: US 6368600-A 7 09-APR-2002;
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Pred. No. 9e-108;
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Sequence
AR204531
                              Chandrashekar,R. and Morales,T.H. Parasitic helminth cuticlin nucleic Patent: US 6368600-A 16 09-APR-2002;
                                                             Unclassified
                                                                      Unknown
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                                                                                             AR204531.1
                                                      (bases 1 to 892)
290
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                      Location/Qualifiers
organism="unknown"
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Similarity

39.7%; 78.1%;

Score Pred.

461; No.

DB 6; .3e-97;

Length

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RESULT 9
AR204532/c
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Sequence 18
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Chandrashekar, R. and Morales, T.H.
Parasitic helminth cuticlin nucleic
Patent: US 6368600-A 18 09-APR-2002;
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                                        investigating 1
Science 282 (5:
99069613
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  2 (bas
Sims, M.
                                                                Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consoscience 282 (5396), 2012-2018 (1998)
                                                                                                                                                                               Z50044.1 GI:899234
HTG; Cuticulin; Elongation
factor; Phenylalanyl-tRNA s
                                                                                                                                                                                                                      Caenorhabditis elegans Z50044
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             The C.elegans Sequencing Consortium.
2 (bases 1 to 25823)
                                                                                                     none
                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z66522.

The true right end of clone F22B5 is at 16002 in sequence Z66523.

The true left end of clone M05D6 is at 25723 in this sequence. The true right end of clone F14E5 is at 4610 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (13-JUL-1995) Nematode Sequencing Project, Sanger
Submitted, Hinxton, Cambridge CB10 15A, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 266523.

For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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IMPORTANT: This sequence is not the entire insert of clone F22B5. It may be shorter because we only sequence overlapping sections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The end of this sequence (25723. .25823) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neighbouring submissions.
The true left end of clone F22B5 is at 24607 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             once,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           name=F22B5
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                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA90354.1"
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EPTLGFDIKTVHFKDFQLNLMDVGGQKSLRSYWKNYFESTDALIWVVDSSDRERLLQC
                                                                                                                                                                                                (ADP-ribosylation factor E-value=2.9e-85, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score=95.9, E-value=2.6e-25, N=1
CDNA EST yk390d8.5 comes from th
CDNA EST yk499d6.3 comes from th
CDNA EST yk390d8.3 comes from th
CDNA EST yk499d6.5 comes from th
                                                                                                   /protein_id="CAA90353.2"
/db_xref="GI:14530408"
                                                                                                                                                                         /codon_start=:
                                                                                                                                                                                                                                                               /note="contains similarity to Pfam domain:
                                                                                                                                                                                                                                                                                                       /gene="F22B5.1"
                                                                                                                                                                                                                                                                                                                       oin(1870. .2158,2209. .2339,2534. .2668)
                                                                                                                                                                                                                                                                                                                                                               /gene="F22B5.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recognition motif. (a.k.a. RRM, RBD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains similarity to Pfam domain: PF00076 (RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join(411. .462,584. .663,745. .1127,1216. .1471)
/gene="F22B5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F22B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oin(411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 25823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .462,584. .663,745. .1127,1216. .1471)
2B5.2"
                                                                                                                                                                                                                                                                                                                                                                                             .2158,2209. .2339,2534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from this gene
from this gene
from this gene"
                                                                                                                                                                                                                              family),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this
                                                                                                                                                                                                                                 Score=295
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gene
                                                                                                                                                                                                                                                                                                                                                                                             . 2668)
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                                                                                                                                                                                                                                                               PF00025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain)),
                                                                                                   CDS
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complement(join(12240. .12394,12467. .1254)
13262. .13392,13465. .13524,13876. .14032))
/gene="F22B5.6"
                                                                                complement(join(12240. .12394,1246
13262. .13392,13465. .13524,13876.
/gene="F22B5.6"
                                                                                                                                                                                                     GGCVDSKYAAVWRKVLHTKVRGPTYYVSHYKPDEVFNPELEFDDVVKFSDVPVEHVVK
YDNS1FPYERKEYILAKFKNGVGRVAYNKSGEVIGIGLVSTESSGNCEIGPIYCDNKN
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EQIKQFQKLVGDFNDIKLLKETMKDNYQLYLLCHKAKNSIAALCYNFNLNSNVMSIYV
SDSTVLSGTQSITYKSLNRSIPDFQTFGLSYQPDNTYNLLPHLMHEMATDFKSVKMNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(10849. .10984
11578. .11832,11917. .12154))
/gene="F22B5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(10849. .10984,11033.
11578. .11832,11917. .12154))
/gene="F2285.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA EST yk304c8.5 comes from this gene cDNA EST yk594h3.3 comes from this gene cDNA EST yk594h3.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVSFHPOFVTKVDRAKRVQCFYMBADKTVSTQIEVSDLTTAFQTQVVPMPICKYEILN
GGPTGEPVQFATIGQQVYHKMYCDSETVDTFCAVHSCTVDDGNGDTVQILDENGCAL
DKFLLNNLEYETDLMAGQEAHVYKYADRSQLFYQQUISITVKBENEECARPTCSEPQE
FGAVKQANQTAQFFRVLKKRSAPVMENILDVRAELTTLEVLEGNLPSSLTQAQALVAS
REIGEDSFRQELCISSFHISVTVFFGLTVFVAIFITVMIVSRMMVPSDKMQSAC"
                                                                                                                                                                             PDGLNFSKVFVSSNPSNAPC"
                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA90357.1"
/db_xref="GI:3876229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAEIWLDRSNSKAPWDWERLRDTYWKMPTVAFDLDGRTRKRCELMEQLQDEMLEAAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSLSKAPRKTMFRFVLSRNASTSNVPSPARIQLKKPAEAGHFQY
SRNWSRDPRFVKVAIQKGDTPYQFLVRRLGHAYEVYPLFVLTAAWFVLFCSASYWSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(9691. .9890,9940. .10234)
/gene="F22B5.4"
/note="cDNA_EST_yk304c8.3_comes_from_this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:Q19707"
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TRNAFEGHVYVKGLFDQQECRNDEGGRQVAGIELPFDTCNVARTRSLNPKGVFVTTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA90356.1"
/db_xref="GI:3876228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q19708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA90355.1"
/db_xref="GI:3876227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(9691. .9890,9940. .10234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_sta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGDRLVQAMTWLCDDVGSRLFILD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {f SEELKKLLGEERLAGASLLVLANKSDLPGAIDVNSIAQVLDLHSIKSHHWKIFSCCAL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F22B5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NA EST EMBL: T01970 comes from this gene NA EST CEESY90RB comes from this gene NA EST EMBL: T00412 comes from this gene NA EST yk386c7.3 comes from this gene NA EST yk386c7.3 comes from this gene NA EST yk396c1.3 comes from this gene NA EST yk594b12.3 comes from this gene NA EST yk543g2.3 comes from this gene NA EST yk543g2.5 comes from this gene NA EST yk543g1.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST yk543g2.5 comes from this gene EST yk595c10.1.5 comes from this gene EST yk590c10.5 comes from this gene EST yk652b8.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .10984,11033.
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                                                                                                               7. .12541,12691.
.14032))
                                                    .12541,12691. .12784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .11343,11397.
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Query Match
Best Local
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                                                                                                        3631 TCTTACCACCGCTTTCCAAACCCAGGTTGTTCCAATGCCAATCTGTAAATACGAGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4051 CAGTAAACTTCAACACACGTAATGCCTTCGAGGGACACGTCTACGTTAAGGGACTTTTCG 3992
                                                             474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
GGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCA
                                                                                                                                                                                                                                         TGTTCAATGCTTCTACATGGAAGCCGACAAGACAGTCTCTACCCAAATTGAAGTCTCTGA
                                                                                                                                                                                                                                                                                    AGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGAGTTGAGGTATCTGA 413
                                                                                                                                                                                                                                                                                                                                                                              TTGATATCAACTAGAAGCTTCTCGTTAAAAAAATGCAAATTGAATTTCCAGTGCCTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAACAAGAATGTAGAAATGACGAAGGAGGTCGTCAAGTCGCTGGAATCGAACTTCCAT 3932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Le Filinited s...

Also Prot accession

CDNA EST yk28d8.3 comes from the comes from the comes from the comes from the comes of the come of the come
                                                                                                                                               AATCACAACTGCTTTTCAAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAACTGTCGTCGTCTTTTCCATCCCCAATTTGTCACCAAGGTTGATCGGTAAGACTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAACTTCTGTAATTTTTAAGGAATGCTTCTTGAAGGTTTAGGATACCGAAATTATAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAAGAAGGTTGCCGTAATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCAT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JULII(15384. .15575,15622. .16479,16527. .17105,18608. .1
18794. .18946,18996. .19449,19497. .19843,20042. .20554,
20672. .21600,21677. .21812)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="Sptrembl:Q19710"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(15384.
18794. .189
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/db_xref="GI:3876230"
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18946,18996. .19449,19497. .19843,20042. .20554,
21600,21677. .21812)
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yk28d8.5 comes from this gene
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Pred. No. 4.
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IMPORTANT: This sequence is not the entire insert of clone C47G2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                               Direct Submission
Submitted (27-APR-1995) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CBLU 15A, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consorscience 282 (5396), 2012-2018 (1998)
neighbouring submissions
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                       available information.
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Z49125
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The true left end of clone T24F1 is at 34731 in this sequence. The true right end of clone T05B9 is at 12750 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For a graphical representation of this sequence and its analysis
see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The true left end of clone C47G2 is right end of clone C47G2 is at 6388
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join(15433
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/chromosome="II"
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                                                                                                                                                                                                                                                                                                                                                                             join(15433. .15770,16205. .16531,16772. .17108)
/gene="C47G2.2"
/note="contains similarity to Pfam domain: PF00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to cuticulin
                                          /protein_id="CAA88935.1"
/db_xref="GI:3875031"
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/db_xref="SPTREMBL:018694"
/translation="MLFSMESILSSTKPKLEPPPKLEPEVTINEQVVDLPRSNTRLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [GFASFLGIGTIVATALSATIFYVARPTSHKH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA EST yk146a2.5 comes from this gene NA EST yk16a2.3 comes from this gene NA EST yk262c12.3 comes from this gene NA EST yk262c12.5 comes from this gene NA EST yk265h3.5 comes from this gene NA EST yk278g8.3 comes from this gene NA EST yk278g8.3 comes from this gene NA EST yk278g8.5 comes from this gene NA EST yk278g8.5 comes from this gene NA EST yk23g8.5 comes from this gene NA EST yk39e8.5 comes from this gene NA EST yk39e8.1 comes from this gene NA EST yk380a11.3 comes from this gene NA EST yk380a11.5 comes from this gene
                                                                                                              ad domain), Score-222.2, E-value-2.5e-63.

NA EST EMBL: 701618 comes from this gene
NA EST yk123h2.5 comes from this gene
NA EST yk22h2.3 comes from this gene
NA EST yk268f8.3 comes from this gene
NA EST yk268f8.5 comes from this gene
NA EST yk474g11.5 comes from this gene
NA EST yk474g11.5 comes from this gene
NA EST yk637f8.3 comes from this gene
NA EST yk637f8.3 comes from this gene
NA EST yk637f8.3 comes from this gene
NA EST yk677a12.3 comes from this gene
NA EST yk677a12.5 comes from this gene
NA EST yk677a12.5 comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2679,2992. .3217,3898. .4636,4687.
;2.1"
                                                                                                                                                                                                                                                                                      ty to Pfam domain: PF00250 (Fork
2, E-value=2.5e-63, N=1
es from this gene
from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .16531,16772. .17108)
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31534. 31033, 3298. 3321, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233, 3233
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complement(join(24417. 24975,25043. 25176,25237. 25522,
25668. 25907,25967. 26049.75,25043. 25176,25277. 26608,
26681. 26785,26846. 26914))
/gene="C47G2.4"
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//gene="c4762.4"
/note="similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /TIABS|ation="MGTISLAYQLF|VFLLTSYLLNKYSTIRKQNPIVTISTFIGWYF
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TLSPAAFVTEXASTRFHYKYTOGVAFGIIVYLLTSAYFTIFRLQIYKYYHLDPNGHTD
ENSILFSAILLCRLTPPICLNRLGMHHNDSHLSMAKSFGIETQFTKLMGHLDVIPILA
ENSILFSAILLCRLTPPICLNRLGMHHNDSHLSMAKSFGIETQFTKLMGHLDVIPILA
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RRKRYKKNSDTYHEMMSHHPMPFPPFLPQGMPFPPRMHPMANIPMLGHPMNPRAVPN
MPAFFIPQNIDSQKLLSMMASRIMPMDAPVSSGQKRTSSSSSPNENGSSAVSDKLSA"
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/codon_start=1
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/gene="C47G2.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(30076. .30134,30184. .30492,31050. .31274,31321. .31480,
31534. .31653,31701. .31835,31889. .33104,32160. .32570,
32639. .32935,32998. .33215,33263. .33651,33802. .34049)
/gene="C4762.5"
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SIKRSNDRSQRTQNWTNSFGSSNAGNGSTTSKEKRSNKNDEERPMLEDDDEEVEESST
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/db_xref="GI:3875032"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(30076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     076. .30134,30184. .30492,31050. .31274,31321. .
.31653,31701. .31835,31889. .32104,32160. .32570
.32935,32998. .33215,33263. .33651,33802. .34049
yk486d7.5 comes
yk513g7.5 comes
yk615h7.5 comes
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LOCUS
DEFINITION
ACCESSION
                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                         CELCUT1
                                                                                                                                                                            RESULT 12
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Matches
      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 TACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 409; Conserv
                                                                                                                                                                                                                                            CGCTGCTCCAC
                                                                                                                                                                                                                                                                                                                                                          TTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGC 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGCATCACAGCTTTTCTA 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTTGGAATATCCAACAGA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCATCGGACAACAAGTCTATCACAAATGGACTTGCGATTCTGAGACCACCTGACACCTT
CELCUT1
2310 b)
C.elegans cuticlin 1 (cut-1) gg
M55997.1 GI:156271
cuticle protein; cuticlin 1.
C.elegans DNA.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATG 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGATGGCTGGCCAAGAAGCTCACGTCTACAAATATGCCGATCGCTCCCAACTCTTCTA 4302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACGAAGAAGGATGTGCTCTTGACAAGTTCTTGCTCAATAACTTGGAGTACCCAACTGA 4242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCGCCGTCGTTCACTCTTGCACTGTCGATGATGGTAATGGCGACACCGTTCAGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAGTCTGCAAATACGAGATCCTTGACGGAGGACCATCCGGACAACCAATCCAGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCACACAGATCGAAGTCTCGGATCTCACCACTGCCTTCCAGACCCAGGTCGTACCAAT 4002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGAT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTAAAATTTCCAGCGCCTACCGTATCCAATGCTTCTACATGGAGTCCGACAAGACTGT 3942
                                                                                                                                                                                                                                                                                       AGCTGCGCAAC 880
                                                                                                                                                                                                                                                                                                                                 CTCAGAGCCACAAGGATTCGGAGCCGTCAAACAAGCTGGTGCCGGAGGAGCTCATGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                     TCAATGCCAAATCTCCATCACCATCAAGGACCCAGGAAGCGAATGTGCCCCGTCCAACTTG
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KEWMISBNLFEKIVDKNRESSTDDEKECLAEVYCEILERLDKLYIMESKVDELHAKS
MDETLIAKIADULIVEEGCPAEELYKKSALISASAKILEAFIKTUTSKANPAQQLEEI
ERNILEERHYSYGLMRFCMDNIDYEHSYQPDFBIVEGILANRLPNILQTVLROIEAN
GSVWOPLLRLIELCNTNCMSTHEKIAVAFRSLPFINLIKARKMLPRASVLHCLLVKV
VILLHSSFPCDELSPAAEYLLTEGGLIQNIVDTATSPNPGSSVACSGLRSFNQNLGD
AINRAKKAGIENQKLLAILSANNTWTELEDIIHLYNLKHRPQWOHDFNDSSVVSSIRN
DSHGFNDSEENTDASTKFAEMDATSSAKQAFSGFSSPFEPNMQRFSDFEGQFDDTPDE
                                                                                                                                                                                                                                            4433
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ENSLMRLLKTDNFTLEDVLLNEFVVQESRYGKAELVQYITSRENMKALLELSLNPKIN
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/protein_id="CAA88937.1"
/db_xref="GI:3875033"
/db_xref="SPTREMBL:Q18696"
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Pred. No. 1.9e-65;
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TACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAA 777
                                                                                                 GATGATGGTAATGGCGACACCGTTCAGATTCTTAACGAAGAAGGATGTGCTCTTGACAAG 149;
                                                                                                                   GGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA 537
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                                 TGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTC
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                                                                ACCACTGCCTTCCAGACCCAGGTCGTACCAATGCCAGTCTGCAAATACGAGATCCTTGAC 1317
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91323673
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/protein_id="AAA27995.1"
/protein_id="AAA27995.1"
/db_xref="GI:156272"
/translation="RLPYPCFYMESDKTVSTQIEVSDLTTAFQTQVVPMPVCKYEILD
GGPSGQPIQFATIGQQVYHKWTCDSETTDTFCAVVHSCTVDDGNGDTYQILNEEGCAL
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FGAVKQAGAGGAHAAAAPQAGVEEVQAAPVGAAPVAAAAAAAPAVPRATLAQLRL
LRKKRSFGENEGILDVRVEINTLDIMEGASPSAPEAAALVSEESVRRRATSTGISSTP
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/db_xref="taxon:6239"
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GTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA
                                                                    AATGTCCTCGACCACAATGCACAGGAGCCACAAGGATTTGGTGCCATAAAATCTGGACAAG
                                                                                  AATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGG----
                                                                                                                    ATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCG
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Sequence 8 :
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Chandrashekar,R. and Morales,T.H.
Parasitic helminth cuticlin nucleic
Patent: US 6368600-A 8 09-APR-2002;
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Pred. No. 2.8e-62;
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                     GATTGATCAAGAAGCGATCAATTAATTCTGATAATACGGTGGACGTCAGTACCGGTTTTA
                                    GTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA
                                                                GATTTGCTGCTGTAAAATCTGCTGCTGCACCAGCTCCAGAAGCTTCCTTGCTTTCTCCAC
                                                                                                                                                                    ATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCG
                                                                                                                                                                                                  ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGG
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                                                                                                           AATGTCCTCGACCACAATGCACAGAGCCCACAAGGATTTGGTGCCATAAAATCTGGACAAG
                                                                                                                       AATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGG------
                                                                                                                                                       GTGATGCAGTGGAGATTCTGAATGAAGAAGGATGTGCTTTGGACAAATATTTACTCAATA
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                                                                                      ------AGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTC
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Parasitic helminth cuticlin nucleic
Patent: US 6368600-A 10 09-APR-2002;
Location/Qualifiers
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AR204525
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1 (bases 1 to 813)
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Pred. No. 2.8e-62;
0; Mismatches 161
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           Query Match
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Matches 352; Conserv
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Submitted (01-OCT-1996) GA3,
NA 80125, Italy
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cut-1-like genes of Ascaris lumbricoides
Gene 193 (1), 81-87 (1997)
97390131
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Ascaris lumbricoides CUT-1-like
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Timinouni,M. and Bazzicalupo,P.
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Ascaris lumbricoides
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1 (bases 1 to 5792)
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                        Conservative
                                                                                                       /gene="ascut-1"
5064..5070
/gene="ascut-1"
a 1254 c 1213
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join(766. .954,2851. .
/gene="ascut-1"
/product="CUT-1-like c
766. .881
                                                                                                                                                                                /product="CUT-1-like 4694. .5081
                                                                                                                                                                                                                                                                                        HARGQQVILSPANEGICMSPFGFSIFMGLAVALAAAVVVVVSFKLRPQQKA'
                                                                                                                                                                                                                                                                                                        TGQPIQFATIGQQVYHKWTCDSETVDTFCAVVHSCFVDDGSGDTIQILNEEGCALDKY
LLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQITITIKEPNSECPRPTCSEPQGFGA
WRPGGSIAPKKQRRCQLRLIKKSGGDYDNTLDVRTDFSALDISDRDEALPMDLRHKAR
                                                                                                                                                                                                                                                                                                                                                       /product="CUT-1-like cuticlin protein precursor"
/protein_id="AAB66646.1"
/db_xref="GI:1657625"
/translation="MCRAVSFLALFGLAAAIPVDNGVEGEPEIECGPTSITVNENTRN
PFEGHAYVKGLYDQEGCRSDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVIS
FHDLFITK/DRAYRYQCFYMEADKTVSTQIEVSEITTAFQTOIVPMYCRYEILDGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="cuticlin gene; ASCUT-1;
proteins of other nematodes"
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join(882. .954,2851. .3239,3583. .4083,4499.
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/variety="suum"
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/gene="ascut-1"
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                    Score 249; DB 3;
Pred. No. 6.9e-48;
D; Mismatches 150
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                                                                                                                                                                                                                                                     2 (bases 1 to 2584)
De Giorgi,C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2584)

De Giorgi,C., De Luca,F., Di Vito,M. and Lamberti,F.

Modulation of expression at the level of splicing of cut-1 RNA in the infective second-stage juvenile of the plant parasitic nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.artiellia Mtcut-1 gene.
X96677
                                                                                                                                                                                                              Submitted (15-MAR-1996) C. De Giorgi, Dipartimento Biologia Molecolare, Via Orabona 4, 70126, Bari, IT
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Ty
Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
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Meloidogyne artiellia
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/gene="Mtcut-1"
join(<467. .943,1139.
/gene="Mtcut-1"
join(467. .943,1139. .1
                                                                                                                                                                                                 Molecolare, Via Oral
Location/Qualifiers
                                                                    /clone="pUc(3000)"
/clone="mp19(1500)"
/clone=lib="lambda7-2(1)"
/clone_lib="lambda7-2(1)"
join(467. 943,1139. .1735,1825.
                                                                                                                                             /organism="Meloidogyne artiellia"
/db_xref="taxon:42426"
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                                                                      AAGTAAGAAGAAGCACTCACTCTTCAGTAAATACATATGCAAACTTTGAATTGCGAT
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2518. .25
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/translation="MRKLLFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
/translation="MRKLLFAIGVFVALNAIFTVRAIPVDNGVEGEPEIECGPTSITV
/VIRTRNPFEGHVYVKIDAACROCTYMEADKTVSAQLEVSEITTQCTQTQVVPMPVCKYEI
TVVISHPQFVTKVDRAYRVQCCTYMEADKTVSAQLEVSEITTQCTQTQVVPMIVKKYEI
LEGAALGQPIOPATIAQQVYTSGTCDSETIDTFCAVVHSCVVDBGNGDTVQILINEGSC
ALDKFLLNULEYPTDLTAGQEAHVYKYADRSQLFTQCGISTITKEPHSECARPKCAEP
SGFNAVKVGAGGAGAGAPPAAAAATPPPAAAPPAPIAPAIFARHHHLLMENLSAEPQRRFIYQGGQQV
RRAAPPGEQVLDVRTENNALDISDKPFNLPAHIRHHHLLMENLSAEPQRRFIYQGGQQV
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/gene="Mtcut-1"
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/protein_id="CAA65452.1"
/db_xref="GI:2648041"
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/gene="Mtcut-1"
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/codon_start=1
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Pred. No. 2e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cut-1-like genes are present in the filarial nematodes, pahangi and Brugia malayi, and, as in other nematodes, components of the cuticle
                                                                                                                                                         Submitted (06-NOV-1998) Devaney University of Glasgow, Bearsden
                                                                                                                                                                                                                                                                                                                          Onchocercidae; Brugia.

1 (bases 1 to 637)

Lewis, E., Hunter, S.J., Tetley, L., Nunes, C.P.,
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Brugia malayi
                                                                                                                                                                                      Direct Submission
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99339397
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/gene="cut-1"
/number=1
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                                                      /gene="cut-1"
                                                                                                               /organism="Brugia
                                                                                                                                          Location/Qualifiers
                                                                                     /clone="cut-1"
                                                                                                  /db_xref="taxon:6279"
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Best Local Similarity 68.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CATAGTAGATGGTGACAAATATTTTAGATTTTGGATGGTGGACCAACCGGACAGCCAATT
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                                                                                                                                                                                                                           CCAACAGAT 690
                                                                                                                                                                                                                                                                     GAAATTCTGAGTGCAGATGGTTGTGCTCGATAAATACTTGCTGAATAATTTGGAATAT
                                                                                                                                                                                                                                                                                                                             GATACCTTCTGCGCAGTTGTCCACTCCTGCTTTGTGGATGATGGCAACGGTGATACGGTG
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                                                                                                                                                                                                            CCGACAGGT 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCTATATGGAAGCTGACAAAACGGTCAGCACCCAGATTGAGGTGTCTGAAATCACAAC 120
                       BPA012618
Brugia pahangi cut-1 gene, partial.
AJ012618
AJ012618.1 GI:3858956
cut-1 gene; cuticlin.
Brugia pahangi
Onchocercidae;
1 (bases 1 to
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/translation="VISFHPLSVTKVDRAYRVQCFYMEADKTVSTQIEVSEITTAFQT
QIVPMPVCKYEILDGGGPTGPATTIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
GDTVEILSADGCALDKYLLNNLEYP"
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/gene="cut-1"
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/protein_id="CAA10074.1"
/db_xref="GI:3858955"
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358)
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Pred. No. 3.7e-34;
0; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                             ACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGATGGTAACGGTGAT 615
                                                                                                                                                                                                              GAATATCCAACAGAT 690
                                                                                                                                                                                                                                                                                  ACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTG 675
                                                                                                                                                                                                                                                                                                                            ACCGTTGATACCTTTTGCGCAGTTGTCCACTCCTGCTTTGTGGATGATGGCAACGGTGAT 120
                                                                                                                                                                                               GAATATCCAACAGGT 195
                                                                                                                                                                                                                                                              ACGGTGGAAATTCTGAATGCAGATGGTTGTGCTCCTCGACAAATACTTGCTGAACAATTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devaney, E. cut-1-like genes are present in the filarial nematodes, pahangi and Brugia malayi, and, as in other nematodes, components of the cuticle Mol. Bicchem. Parasitol. 101 (1-2), 173-183 (1999)
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                               Caenorhabditis elegans
Z81088
Z81088.1 GI:1627965
                                                   HTG
                                                                                                              CEF53F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-NOV-1998) Devaney E., Veterinary Parasitology, University of Glasgow, Bearsden Road, Glasgow, G61 1QH, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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/number=1
350. 356
/gene="cut-1"
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192. .349
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/db_xref="GI:3970656"
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join(<1. .191,350. .>356)
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join(<1. .191,
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/db_xref="taxon:6280"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="cut-1"
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/translation="PIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEI
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87.7%;
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Pred. No. 3.6e-26;
0; Mismatches 24
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                                                                                             39478 bp DN cosmid F53F1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        For a graphical representation of this sequence and its analysis see: - http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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Direct Submission
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investigating biology. The C. elegans
Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                  /db_xref="Sptrembl:Q9xym/"
/translation="MONKEIERTLEDYFPKGFLISESSKYDCHLEDMHLVIQLLLATL
/translation="MONKEIERTLEDYFPKGFLISESSKYDCHLEDMHLVIQLLLATL
AVMPVPIQNSLYGDVLCDSRTISVQIKTEKPFYGVIFYKDEASEEVCTSRG7GFLS
AFLEIEIGLGGALRQBVLMFKGLAVRTITISFHPYFTTKVDRTYNLLCYRESQVFY
ANNISVDEISTISYNVNLTMPTCTYQILSGGPFGEPVEFGLIGQQVYHQWKCNNDKGM
INLIKEDSFCMVVHTCSVDDGRGETSFLIDSNGCSIDKFLLSNLEYPGNLLAQGEAHY
     cDNA EST yk473d8.3 comes cDNA EST yk473d8.5 comes
                                                                                                                                                                                                                                                                                  YKFADRDALFFQCQISITVKEPDQECVRPICEDVEGGGAPVVGPPPYGMISKNLVNIW QKNSFLTFFKSPYMYVVGITNYHNKAIQKL" join(17396. .17599,17683. .17926,17977. .18146,18197. .182
                                                        (Aldo/keto reductase family),
E-value=1.7e-143, N=1
                                                                                                                   /note="contains similarity
                                                                                                                                             /gene="F53F1.2"
                                                                                                                                                                           18339. .18524)
/gene="F53F1.2"
join(17396. .17599,17683.
18339. .18524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB03124.1"
/db_xref="GI:3877456"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(14923. .15347,15663. .15774,15835. .15984,
16033. .16271,16318. .16486))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(14923..15347,15663..15774,15835.
16033..16271,16318..16486))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted using Genefinder
similar to cuticlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F53F1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F53F1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="F53F1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans'
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .39478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consortium
     from
                                                                                                                                                                                                     .17926,17977.
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                             this gene
                                                                                     Pfam domain:
Score=488.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis
gene"
                                                                                                                                                                                                     .18146,18197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for a small
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/note="predicted using Genefinder similar to cuticlin cDNA EST EMBL:T01107 comes from this gene; cDNA EST EMBL:T01107 comes from this gene; cDNA EST yk60a10.3 comes from this gene; cDNA EST yk90a9.3 comes f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
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CDNA
                                                                                                                                                                                                                                                                                            /gene="F53F1.5"
join(25572. .25660,25850. .26408)
/gene="F53F1.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:Q9XVM6"
/translation="MQKIVIFFAAIAVSQAFLLPSGGGGGGGCAPPPPPPPCGCGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAB03125.1"
/db_xref="GI:3877457"
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MYLIHYPKSFDYGDQDPMNKTLRIATWNDLWECKNAGKIRSVGVSSFEIRHLEELKDL
GKNFPPCCNQVEYHPHFTREELKNYCKSEGIFFQAFSSLARHNETLLSSEIITRLAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(25572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-value=4.4e-135, N=1"
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join(18714. .18887,18935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EESLQSLQTDYIDMYLVHYPKPNDSDNDDVNNAEYRKIAYEVLEEAKAAGKVRSIGVS
NYEIVHLEELKTYAKVPPCANQLEYHPHFARIPLQKYCKEKNIFFQAFSSLARHEPKL
IEDPVVVELAKKHNTSVPLVLLAWALRQNVGIVPKSVTPSRIVENFKVIDIALTPEDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YHVPKTTVLLSWATSQKVGIIPKSTNPERLAQNLKTVLLEEEEVKKICNLNLDKHYVR
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/translation="MSIKLNTGYDCPLIGLGTYKIIGDQVLPVLDAALTAGYRLFDTA
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/db_xref="GI:3877460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(18714.
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/gene="F53F1.3"
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/translation="MSDSFANVPGGSQKLNSGYNIPFVGFGTYKVTGENVPPAIDAAL
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/db_xref="GI:3877459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NA EST yk122a3.5 comes from this gene
NA EST yk122a3.5 comes from this gene
NA EST yk122a3.5 comes from this gene
NA EST yk121a3.3 comes from this gene
NA EST yk151b10.3 comes from this gene
NA EST yk191d9.3 comes from this gene
NA EST yk234b3.3 comes from this gene
NA EST yk3010g2.3 comes from this gene
NA EST yk34b16.3 comes from this gene
NA EST yk341b10.3 comes from this gene
NA EST yk341b10.3 comes from this gene
NA EST yk341b10.3 comes from this gene
NA EST yk341b10.5 comes from this gene
NA EST yk300g2.5 comes from this gene
NA EST yk301b0.5 comes from this gene
NA EST yk301b0.5 comes from this gene
NA EST yk301b3.5 comes from this gene
NA EST yk301b3.5 comes from this gene
NA EST yk301b3.5 comes from this gene
NA EST yk301b0.5 comes from this gene
NA EST yk301b3.5 comes from this gene
NA EST yk30b3.5 comes from this gene
NA EST yk506b3.5 comes from this gene
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08,20072. .20251)
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Score=460.5,
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Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      557 CCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATA 616
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TTCGACCACAATGTTCAGAACCACAAGGATTCGGAGC 833
                                                                                                                                                      CACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTG 796
                                                                                                                                                                                                                                                                                                         AATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATCGAT 736
                                                                                                                                                                                                                                                                                                                                                                                        CCTCATTTCTCATAGACTCGAATGGGTGCTCAATTGATAAGTTTCTATTGTCGAACCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAAGACTCATTCTGCATGGTAGTTCACACGTGTTCTGTTGACGATGGACGAGGTGAAA 15291
                                                                           ATGCTCTTTTCTTCCAGTGTCAGATATCAATTACCGTCAAAGAGCCAGACCAGGAATGCG 1511:
                                                                                                                                                                                                                                     AGTATCCGGGAAACTTACTCGCTGGGCAAGAAGCTCATGTGTATAAGTTTGCTGATCGAG 15171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comes from this gene; cDNA EST yk60a10.5 comes from this gene; cDNA EST yk80e5.5 comes from this gene; cDNA EST yk80e3.5 comes from this gene; cDNA EST yk80e3.5 comes from this gene; cDNA EST yk90a3.5 comes from this gene; cDNA EST yk10a5.5 comes from this gene; cDNA EST yk126b3.5 comes from this gene; cDNA EST yk126b3.5 comes from this gene; cDNA EST yk258a5.3 comes from this gene; cDNA EST yk258a5.3 comes from this gene; cDNA EST yk30p10.3 comes from this gene; cDNA EST yk40p16.3 comes from this gene; cDNA EST yk40p16.5 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107.4; DB 3;
Pred. No. 1.1e-14;
0; Mismatches 106;
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-NOV-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, Submitted by:
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St. Louis, MO 63110, USA
e-mail: jspieth@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis briggsae"
/strain="GujArat G16"
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                                                                                                                                                                                                                                                                                                                                                 Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IT may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone E04D5 is at 1 in this sequence. The true right end of clone E04D5 is at 2110 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-0CT 1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CBI0 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
the specified clone. It may overlapping sections once, overlap between neighbouring
                                                                                                                                                                                                                                          sequence 248585.

The true left end of clone ZK673 is at 31437 in this sequence. The true right end of clone T09F3 is at 11412 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consor Science 282 (5396), 2012-2018 (1998) 99069613 9851916
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                      For a graphical representation of this sequence and its analysis see: _http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                              sequence 248585.
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                                                                       This sequence is NOT necessarily the entire insert of
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                  It may be shorter because we only sequence once, or longer because we arrange for a small
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CDNA EST yk598all.3 comes from this gene; yk640h2.3 comes from this gene; choke Est yk656h4.3 comes from this gene; choke Est yk656h4.3 comes from this gene; choke Est yk650h4.3 comes from this gene; choke Est yk650h4.
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cDNA EST yk159c6.5 comes from this gene; cDNA EST
yk162e2.5 comes from this gene
cDNA EST yk164e3.5 comes from this gene; cDNA EST
yk268c5.5 comes from this gene
cDNA EST yk519a6.3 comes from this gene; cDNA EST
yk533e1.3 comes from this gene; cDNA EST
yk536e6.3 comes from this gene; cDNA EST
yk536e6.3 comes from this gene; cDNA EST
yk578a6.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA EST yk533e1.5 comes from this gene; cDNA EST yk556e6.5 comes from this gene cDNA EST yk578a6.5 comes from this gene; cDNA EST yk58lh3.5 comes from this gene cDNA EST yk59ba11.5 comes from this gene; cDNA EST yk59ba11.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yAJOJOBN 5 comes from this gene CDNA EST yk256f12.3 comes from this yk256f12.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yk402312.5 comes from this gene cDNA EST yk375c1.3 comes from this gene; cDNA EST yk375c1.5 comes from this gene; cDNA EST yk374f8.3 comes from this gene; cDNA EST yk374f8.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yk454d9.5 comes from this gene cDNA EST yk350b11.3 comes from this gene; cDNA EST yk350b11.5 comes from this gene; cDNA EST cDNA EST yk413f5.3 comes from this gene; cDNA EST yk402d12.3 comes from this gene; cDNA EST yk402d12.3 comes from this gene; cDNA EST yk402d12.5 comes from this gene; cDNA EST yk402d12.5 comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA EST yk117a5.5 comes from this gene; cDNA EST yk132f3.3 comes from this gene; cDNA EST yk132f3.5 comes from this gene; cDNA EST yk132f3.5 comes from this gene; cDNA EST yk135c2.5 comes from this gene; cDNA EST yk135c2.5 comes from this gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA EST yk365e8.3 comes from this yk365e8.5 comes from this gene
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                                                                                                                                                                                                                                                                                                                                                      cDNA EST yk663a4.5 comes
                                                                                                                                                                                                                                                                                                                                                                                             cDNA EST yk640h2.5 comes from tyk656h4.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA EST yk454d9.3 comes yk454d9.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA EST yk459b6.3 comes from this yk459b6.5 comes from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA EST yk165g1.5 comes from this gene; yk165g1.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(6082. .6250,6307. .6379,6432. .6509,6564. .
6750. .6930,7003. .7283,7337. .8179,8228. .8326)
/gene="E04D5.1a"
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                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="E04D5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from this gene
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NUPRYSLADCKHUSTFSAPKEASWEPOPSDDESLAARMVGSEVEFYTNUSEDRYDHKL VEKGATNFALSPGPAPNHVAVYVPAVGSTPARVRVHRVSEPVVGNRTFFKSDKAVM TWNQRGQSLLILASVEVDKTNQSYYCEQSLYLINIQSGESVVVPLEKKGPIYAAKWNP NGREFAVCYGYMPAKVTFYNPRGVPIFDTIEGPRNDVFYNAFGNIVLICGFGNIAKGK

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BASE COUNT
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                                                                                  10458
                                                                                  ω
                                                                                                                             /db_xref="SPTREMBL:Q19054"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKLAPVFKFADKAGLYFNCQIQLTIKDVNYGCSNTQPQCPTSQYVVEPAQKTTETAEP
YPYDSHESGYPTRPANYPVASSRYPIPTTQAPASYPSSPAPPPPGADIDNGYPEPQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSEPSCMTVGDGKTGHRFEVRHDSCGVRRQREINGVVISATVIISFHSIFITKIDRAY
RVSCFYVEGTKKVHNHVDISALTTQLLESETQLPVCRYEILNEAGGSPIKYARIGDQV
YHKMTCVAELENVYCMKVHSCTVYDGQGGPPVTVIDANGCSVDGVILQNLEYTSDLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Join(25834. .25873,27277. .27512,27582. .27721,27768. .28158. .28410,28491. .28811,29092. .29213)
//gene="E04D5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juin(25834 . 25873,27277 . 27512,27582 . .2
28158 . .28410,28491 . .28811,29092 . .29213)
/gene="E0005.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q19055"
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FNERGRIVTVIFVCFFSVAIRIPVLYAMKVKFFLCDDVFRSESLDGTPFAATEAVEV
FNERGRIVTVIFVCFFSVAIRIPVLYAMKVKFFLCDVFYADIHVRVKKAGEVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(8619. 10089. 10283,10330. .
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CDNQVTRVFEIATNKEILCVELKRTRKILFSPKDNFLLTFEPWAVYGPKRTKSQNQMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(8619. .8761,8813. 10089. .10283,10330. .10614,10730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTVLRMESTYQRSQLQKKHRGSLSFRMMSRWLQEWLAVKSSFIQTCLSTVTTTSLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(6082. .6250,6307. .6379,6432.
6757. .6930,7003. .7053)
/gene="E04D5.1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQERKAFQLKKKVEEIKVLKQRVANGDQLQPNQMEKIQRENEYLSELSKLTI"
join(6082. .6350,6307. .6379,6432. .6509,6564. .6696,
                                                                                                                                                                                                                   /protein_id="CAA91281.1"
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join(29675. .29840,31127. .31214,31267.
                                                                                                                                                                                                                                                                                                                                                                                                                                {	t VTVGDIDLPERGILVFGLEEMEDGETTNAGDHGATRALREARNSQEKTCFSTSRMYFT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA91280.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLPENYVLLQVAADVIKESLIHRSSRSKRSQLRNAIYTMLAIVTSYLVCNGVHLFLTI
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                                                                                                                                                                                                                                                                                             /gene="E04D5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAETPENAYDGIVGFNDTEQPFTTSAAYTEDGVYSRLIKRNVVESTEQINASNKKRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q19053"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDFHVITAIQMMFPFVVLLLLNLTIIKRLVAEKRENMYPILRGAGTTTEVKKASFVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA91282.1"
/db_xref="GI:3875454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="E04D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAC42280.1"
/db_xref="GI:14530389"
                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                         /gene="E04D5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="similar to cuticling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LERFDPSYLYESTDRMQSSTFYIVLSDTVSICYMASSAIRIFIYAKCNPKLRQEITDY
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7.2%;
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                                                                               5636
                                                                                                                                                                                                                                                                                                                            .29840,31127.
Score 83.8;
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.10614,10730.
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Length 31536;
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. .10935,11582.
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..10935,11582..11629,
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RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCAAATTTGCTGACAAAGCTGGGCTTTATTTCAATTGTCAAATTCAATTAACAATCAA 28082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTTGCGTTGCTGAACTTGAGAATGTGTACTGTATGAAAGTTCACTCATGTACGGTTTA 27902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAACCAAATAGCGAATGT 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGATCCTTCAGAATCTTGAGTACACCTCTGACTTGACAGCTGGAAAACTCGCACCAGT 28022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGATGGTAACGGTGATACTGTGGAAATTCTAA----ATGCTGATGGATGTGCTCTTGATAA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATGGACAAGGTGGACCACCAGTAACTGTCATTGATGCCAATGGATGTTCTGTAGATGG 27962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGACGTAAATTATGGATGT
                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-0CT-1996) Nematode Sequencing Project, Sanger Submitted, Hinxton, Cambridge CB10 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                      current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone F53B6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
The true left end of clone F32H2 is at 32306 in this sequence. The true right end of clone T08G11 is at 7984 in this sequence. The start of this sequence (1. .105) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consor Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                         neighbouring submissions.
The true left end of clone F53B6 is
right end of clone F53B6 is at 5116
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                                                                 sequence Z81523
                                                                                                                                                                                                                                                                                                                                                available information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1
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(bases 1 to 32412)
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Consortium
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence Z81523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Immunoglobulin domain), Sco
CDNA EST EMBL: 214404 comes fro
CDNA EST yk153a1.5 comes fro
CDNA EST yk195c9.3 comes fro
CDNA EST yk195c9.5 comes fro
CDNA EST yk286g7.3 comes fro
CDNA EST yk286g7.5 comes fro
CDNA EST yk286g7.5 comes fro
CDNA EST yk323a9.5 comes fro
CDNA EST yk323a9.5 comes fro
                                                                                                                         /db_xref="Sptrembl:p00884"
/translation="MKCSYTVUFLLFYLLIASFHVDALSWAAWSPWSSCTKTCGGGVS/
/translation="MKCSYTVUFLLFYLLIASFHVDALSWAAWSPWSSCTKTCGGGVS
RQLRRCLTSKCSGESVRFKVCAOKTCESKSRLARDTICGGEEIVSRGQCEVVCRSRLT
GANFLWRVDDGTPCQAATSRAVCSKGSCQIVGCDGLISSSFREDACGVCGGRGDTCDN
GKFIKKVSEFYTACASNCDDIVDWSGAGRSLASTSQPIVVCVWALTGRVVPEKLCADK
LRFKVEARFCPMLICPSRWMAADWTECVPHCGEGTRKEFYCCVQTAHNVTVHVPDTFC
ENGTRPAAEEMCVSTSCGRWEAGKWSKCTASCGGGVRRRHVACVGGSSDCDEGGRRPQE
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRLVAGEWSTCSSTCGTG
TTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRLVAGEWSTCSSTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLQNDLLHVMNVASWLCITNAIVQIIPSVAGCWYSKLIRK"

complement(join(4270. 4339,4493. 4547,5071. 5295,
5368. .5662,5891. .6148,6204. 66752,6818. .7287,7546. .76:
8104. .8184,12576. .12775,13246. .13384,13931. .14132,
14183. .14294,14341. .14457,14994. .15155,15198. .15311))
//gene.*F5386.2**
                             VMSRTYECVAVNPISSAPIKLPMSECQDQEQPKLFESCEVRSCPLQEDSKLSEDEAPY
QWRYGDWTQCSASCLGGKQKAALKCIQVSTGKSVQWSQCDARRRPPEKSRPCNQHPCP
PFWLTSKYSDCSMSCGSGTARRSVKCAQTVSKYDGADAHIVLRDDRCHFKKPQETETC
      NVVACPATWVSSLNKRHNKIKLNKLKTAQWTECSRSCDSGERRRQVWCEIRDSRGKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(4270. .4339,4493. .4547,5071. .5295,
5368. .5662,5891. .6148,6204. .6752,6818. .7887,7546. .7676,
8104. .8184,12576. .1275,13246. .13384,13931. .14132,
14183. .14294,14341. .14457,14994. .15155,15198. .15311))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSQYAELVSPSLYVDVGRILVIISILSILNYLICFYAIFKEMRCFVTSCAVASIVIAV
MLIIGGCIGLNFRDQLTHYTPLNLKMLTSLRELYGTHDMKGITESWDALQSNFKCCGV
NGTDNAQIWKTSKWYMHQRAFKLLIPESCCIPSEIERCRSNPFDQDAPPPYYTSTCYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity to Human platelet-endothelial tetraspan antigen (SWLPET3_HUMAN), contains similarity to Pfam domain: ppr00335 (Transmembrane 4 family), Score=30.0,
                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB03121.1"
/db_xref="GI:4008366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14183. .14294,14341. .14457,14994
/gene="F53B6.2"
/note="predicted using Genefinder
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/translation="MGALGDSAYGARGRLIKFSYIVTALISILFSISCICYGIWLLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB03120.2"
/db_xref="GI:11065632"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )oin(1863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted using Genefinder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity to Pfam domain: PF00047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1946, 2437. .2628, 2969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from this gene from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score=24.4, E-value=1.7e-06, N=1 es from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3154,3205. .3308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3154,3205.
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gene
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contains similarity to Pfam domain: PF00635 (A sperm protein) domain), Score=74.1, E-value=9. CDNA EST yk193h3.3 comes from this gene CDNA EST yk193h3.5 comes from this gene CDNA EST yk193h3.5 comes from this gene CDNA EST yk411f5.5 comes from this gene CDNA EST EMBL: AW057173 comes from this gene CDNA EST EMBL: AW05732 comes from this gene CDNA EST EMBL: AW057361 comes from thi
                                                                                                                                                                                                                                                                             glycoprotein (SW:12A6_RAT) "
/codon_start=1
/db_xref="Sptrembl:p90883"
/translation="MILSDQNFLQTQMKEPQTAQSKNTESKCEFHGNSNEVKPIGSLN
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GQSIAQCRIHTEKTVPIVKGGEQARMEENEIYAIETGSTGKGYFHDDMETSHYMKNF
ELADEKIPLRLQKSKGLLNLIDKNFATLAFCRCWIDRLGETKYLMALKGKCSYSTASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGVSDKQSNSSKSSKKSSKSSKSRKNRRLDSDAQKKMEKSGKSGKVALIPKTQQTTGS
QVGHSLAEEVNSIKHSKEMNVAPAKLQYQTLGGVNQIELKNTSNERKAYKIKCSDNSL
YRVNPVYGFAEPRSSVKIDVLRLNGEQKTDKLVLLTANANGSTNPHEAFANQAEHREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MRIRSRGQPFRKSKCDQSIDNKNQFEVLKEEARVCASIARTRMLVPLTAIVTTSLPMVAAIAFCAKNRKTVHAKNKNKNKSSKSAKSSKSTRGASKSGKSGKSRRSKAKHSKRSSKSSKKSKKOTSGKGSGKGSKGSKRGGKSSKSKKVKTATTSGSQVSTVSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F53B6.5
23555. .24160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="F5386.4
/note="predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(20516. .20602,20648. .20953,20999. .21424,
21609. .21818))
/gene="F53B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MANQQRIFVFFVVLLFAIVTYAHHSHSYSHSHEHHHHHHGGYYGGGYGGYYGYYGGGYYRQNYWGGRKK"
complement(join(19892. .20022,20241. .20283))
/gene="F5386.8"
                                                                                                                                                                                                    /protein_id="CAB03119.1"
/db_xref="GI:3877451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MVVPLVAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB03117.1"
/db_xref="GI:3877449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGYYQSNYWGKRK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEALLTAPNDEKAREQLRKYGNELVARWDIGHWSECRQKTCHVAGYQARGISCKVTFH
GEIRNVDNSICESLASVRPPETRPCHREDCPRWEASQWSECSSQRCVSSMLAQKRRNV
TCRFTNGTSVDIQHCDITNRPATTMDCPNQNCKAEWRTSDWGSCSSECGTGGVQLRLL
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/gene="F53B6.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCVWISSGRPAGRNCEQMRRPHSARACVADEPLPPCMPTASALYQRDASCQDQSRFCD
IIKLFHSCDSLEVRQKCCSTCTFVERKKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="SPTREMBL:Q9XVN1"
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/translation="MDFGILLVFLMAVAGTFAGISVSFSHSHEFPRHGLLGGGGFNPY
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/db_xref="GI:5824510"
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LQGNVTLNFKYRDFPASRVDLAPKPQIPSTKNRQRVQVSKEDVLREQASVLHKMNVSL
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-19, N<del>-</del>1
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LMLILTLETDRWMAMVGACILQSFAGKIIGKRANLLLNLII"

26802, 26846.

26926, 26974 . . 27107

)oin(26258. .26342,26501.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29771 CATTTTCCTTCACAATGATCACCTCGTTTCATCCATTCTTTGTGACGGGAATGGATCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249207.1 GI:1067021
HTG; ADP,ATP carrier protein; Cuticulin; Cysteine proteinase.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                 available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

This sequence is the entire insert of clone ROTE3. The true right end of clone F41E7 is at 36774 in this sequence. The start of this sequence (1. .115) overlaps with the end of sequence 268106.

The end of this sequence (39633. .39736) overlaps with the start of
                                                                                                                                                                                                                                                               Submitted (05-MAY-1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Nov 21, 1995 this sequence version replaced g1:798823. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
Z49207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cottage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The C.elegans Sequencing Consortium (bases 1 to 39736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F53B6.7"

join(26258...26342,26501...26802,26846...269

join(26258...27384...27459)

z7153...27288,27334...27459)

/gene="F53B6.7"

/note="predicted using Genefinder cDNA EST EMBL:AW057436 comes from this gene cDNA EST EMBL:AW057493 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:Q9XVN0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB03118.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="GI:3877450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74.8; DB 3; Pred. No. 5.1e-07; 0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39736 bp DN cosmid R07E3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 32412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .26926,26974. .27107,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INV 24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                      CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDFSFFSSNRKKL
EQYEEEEGSVEEDMPEDFQHKKPRRSSSASDLGIINREKSDIIDAKLHETNVPEAKQT
                       /db_xref="SPTREMBL:Q21812"
/translation="MIFLVFWFLILLLIFLAVTGKTLGLREYYVNTLVYIFEWGATLN
                                                                       /protein_id="CAA89072.1"
/db_xref="GI:3878960"
                                                                                                                                                                                                                                                                                                                     /gene="R07E3
                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="R07E3.Ś#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="R07E3.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="R07E3"
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IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terminus is glycine rich cDNA EST yk18591.3 comes from this gene cDNA EST yk259b4.5 comes from this gene cDNA EST yk559c11.3 comes from this gene cDNA EST yk574h3.3 comes from this gene cDNA EST yk597h8.3 comes from this gene cDNA EST yk597h8.5 comes from this gene cDNA EST yk597h8.5 comes from this gene cDNA EST yk597h8.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                   13402. .13542,13587. .13696,13745. .1
14541. .14554))
                                                                                                                                                                                                                                                                                               complement(join(11510..11773,12101.
13402..13542,13587..13696,13745...1
14541...14654))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mrvlectluvvaatsaqpfsmgnnnenyydqfgykdaissmsda
kkiamnnexynabsmssfilppffekaedldmkikmgkgdstitulktulllprv
kgqnbftffstytffftgkgftstfftfftftgtattelatttultterk
QqlagrlyqpdmdsgepesaedgidkkktaekvDfttdDnnvsqeadakpDsthengg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(5080. .5246,5409. .5769,5826. .5942,6381. .6905,
6955. .7075,7125. .7448,7495. .7787,7831. .7980,8037.
8222. .8405,8470. .8873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAAPVTAPKPVAPAPSPFGGGGFGGGGGGGGGGGGGGGGGGGGGGGGSGPSVPFDEVEKNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPQGYVGPLPPAPPPPTFRVAPQVPLPVVQTTQTAPKPTLPPTTLPVLTTNKTPRTKD
EGYEQGRDGVKTTFHGDSGVMTGGGHSAPTFDYLNMPSESFGLAPVAPPAPPPPPATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILQGSSASRARAASVRTYEKTKTPNIRDIMADGYSENSLVGFGSQLAREILNPGILK
RDKLTRDKAMAAKLEEAKVRNNAVAESMATGAPLDLSGFPQYQQRPVATNSKLPYFIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSNVETAEVAASAAAAPVALPEPIAPPQIALPQLTPDQISQFMRPVASIVEDMRPILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQPKTTTIVASSTETSTVTTDATEATTTTTAPTTTVATTTTKKRSNIPEAEEDEIEET
AEKTTTKVTEDGPITTEFPEYIKKRNAIVGIKTLTPAQLEAAINAKPIPSSASEASAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEITTTTTKAPTTTTQSTTTTTQLPTTTTTTEPTTTTTTVDPLAENEELEKQAIEVM
KSLDDEERIDAEKNVEVQKRKDERNAARKRINNFLKMMQKARENKNKPHKETTTSLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHVSTTPEESITENTTAEVPASTASTKDTKLSVKIRSEDEKREEDKLSDDEKPNYMKK
LEEIYKKEEELVERELAEMSVAEIFEKEVVIKTTKVTPTSTTTEIPTTTTTEEATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA89071.1"
/db_xref="GI:3878959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(5080, 5246,5409, 5769,5826, 5942,6381, 6905,
6955, 7075,7125, 7448,7495, 7787,7831, 7980,8037,
8222, 8405,8470, 8873)
/gene="R07E3.6"
                                                                                                                                                                                      /note="contains similarity to Pfam domain: PF01553
(Acyltransferase), Score=14.4, E-value=9.4e-05, N=1
                                                                                                                                                                                          (Acyltransferase),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q21811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Serine and threonine rich protein,
EST yk278a10.3 comes from this gene EST yk278a10.5 comes from this gene EST yk486f8.5 comes from this gene EST yk603d8.3 comes from this gene EST yk603d8.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                      1. .12476,12528.
.13863,13912. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .13863,13912. .14026,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .12476,12528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carboxyl
                                                                                                                                                                                                                                                                                                                                      28. .12827,
. .14026,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8174,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8174
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TEVADKEDGHQCQTKQCRLLDDLS"
complement(join(26570, .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(26570. 27330. .27815,27863. .
                                                                                                                                                                                                                                                                                                                                                         /translation="mlinnsgslpltlslyilpdrllnvrffmidrpaktvrepall
TDYISRAFDKMPSSIHLIFLFSQCVVLFSFSQLALSLLSVKTGEEVVDTEAAVTWEDM
VVBDTVEVVIWEEDMVAEVTWEEAAMEVAETWEEDTEEVVTADMVATEVADTEEVVIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="STTREMIL:Q21809"
/translation="MASTSATIDVLETSKKCLAGSAAAAISKTTTAPFDRVKLVLQLQ
/translation="MASTSATIDVLETSKKCLAGSAAAAISKTTTAPFDRVKLVLQLQ
/translation="MASTSATIDVLETSKKCLAGSAAAAISKTTTAPFDRVKLVLQLQ
RQSEFAMAEYNGICISKILEQGAMENGRGWAGVRCLPFHTLNFLAFDIYRNTL
LKNUDRNESFCKFLAGTFVSGGLGGATTLFHLYDFDBATFLALDVKKGSSRKYKGMV
DCLKKIKASEGVASWYKGLSSALQFVIASRAIFFGIFDSIRTSVEDPKSLNFAACWAI
AQISITTSGMYCYPLDTVRRSMMQSGKQIKQYTSTKDCWKTLYKKDGINGFYRGALT
                                                                                                                                                                                                                                                                complement(join(26570. .26749,26841. .26917,27073. .27251,
27330. .27815,27863. .27958,28006. .28071,28119. .28220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="R07E3.1"
                                                                                                                                                                                                                                                    28273. .28295)
                                                                                                                                                                                                                                                                                                                                    eaateweeeavemvdtevvameatweeetwevvvdtdptkedhnnqwedskevmvdnl
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:Q21814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA89074.1"
/db_xref="GI:3878962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(23363. .23562,23642. .23720,23765. .23899,23955. .24269)
/gene="R07E3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poin(23363. .23562,23642. .23720,23765. .23899,23955.
/gene="R07E3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA89068.1"
/db_xref="GI:3878956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(21213. .21359,21654. .21739,21787. .2188
22011. .22170,22220. .22335,22428. .22542,22637. .22779,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E-value=1.7e-68, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(17917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18604. .18751,10
/gene="R07E3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLEEKSSDILNIMQGISEEERDELLKQIDEQDDEEEMIRKISSLKPKFKIGDHDADEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSRSEHHIWFERGEAGDRAKVMDRWREHVNDENKLPIIIFPEGTCINNTSVMMFKÄGS
FEIGSTIYPIAVKYDTRLTDAFWNSSAQSYGRYLWSMMTSWAIICDVWYLPAMTRGEN
EDSISFAKRVKRAIAKKGGLIDLEWDGALKRERVSSKLVTLQQKLYFERLARTTTLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVSVLVDDTLDFITAGMEAVIEDOVTNRFSAAQLPSWNLLSRTKYSFHFFNWQLTLLM
IAGFWFRYYVLVPCRIALFGIAIVLMIVSTSIIGLVPNAKVRKFLNRRCMLMCMRIYS
RAFSSVIRFHDKENRANKGGICVANHTSPIDVMVLSCDNCYAMIGQKQAGFLGFLQTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to cuticulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="R07E3.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="R07E3.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mitochondrial carrier proteins), Score-236.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(17917. .18025,18074. .18331,18378.
18604. .18751,18800. .18877,18947. .19072))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="GI:3878957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'protein_id="CAA89069.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="R07E3.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="contains similarity to Pfam domain: PF00153
EST EMBL: M89104 comes from this gene EST yk68h10.5 comes from this gene EST yk72g11.3 comes from this gene
                                                                                 similarity to Pfam domain: PF00112 (Papain protease), Score=215.1, E-value=3.5e-61,
                                                                                                                                                                          0. .26749,26841. .26917,27073. .27958,28006. .28071,28119. .:
                                                                                                                                                                              .28220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 24269)
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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DEFINITION
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CEM142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                         JOURNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22051
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gene

CDS

gene

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22171 GATGCGCTCTCGACAAATACCTCCTCACAAATCTTGAGTATCCCCACAGACCTGATGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 GATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCGATCACAGTCAAAGAGCCTGGTCTTGACTAT 22017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGGGAAGCCCACGTATACAAATATGCCGATAGAGATAACATGTATTTTGATTGTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGTATTACCATTAAAGAACCAAATAGCGAATGT 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100;
                                                                                Submitted (21-MAY-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 18A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu

On Nov 4, 1996 this sequence version replaced gi:1370039.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones.
dye primer and dye commence.

Exceptions are indicated by an explicit note.

This sequence is the entire insert of clone M142.

The true right end of clone C44B9 is at 5059 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the nematode C. elegans: a pla
investigating biology. The C. elegans Sequencing
Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                        McMurray, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                            The C.elegans Sequencing Consortium. 2 (bases 1 to 36306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99069613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; Cuticulin; Homeobox protein EVX1 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z73428.1 GI:1657678
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Z73428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhabditoidea; Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                      Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yk587h4.5 comes
yk591e7.5 comes
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yk174e6.5 comes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 3; Pred. No. 3.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comes from this gene
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d м142,
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from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39736;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end of this sequence (36203. .36306) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"predicted using Genefinder contains similarity to Pfam domain: PF00092 (von Willebrand factor type A domain), Score-155.0, E-value-4.3e-43, N-1 cDNA EST yk518d1.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-PROT:Q10658"
/translation="MKAEQQQQSIAPGSATFPSQMPRPPPVTEQAITTEAELLAKNQI
TPNDVLALPGITQGFLCSPSANVYNIEFTKFQIRDLDTEHVLFEIAKPENETEENLQA
QAESARVYRYRFAPNFLKLKTVQATVEFKVGDVPITHFMIEHHFFKDRLLKCFDFEF
                                                                                                                                                                                                                                                                                                                                                                    GVGTIDVFTDSVTVLEQEPACQQVTTYSFRFSISTNQKIENS*
join(17427...17468,18628...18766,20758...20)
                                                                                                                                                                                                                                                                                                                                                                                                                                          TVPLSVSMITTVFREQIYQMPQCAYTLRKGAPDGPIVRFATLGESVYHRWECIEVEGA
DKDTFGMLVHSCYVDNGYGDRVDILDSNGCGLDAVLLSTPDYDTSLRLATKPYHVFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÄVEVILLLDASGSIGDDTFKKOLSFAMHLASRLNISEDGSHMÄLIQYAETPKLEFSLG
OFNHFTOLEMAIQRIEYQSGANNTGOALRLTLEKGLOGARPGILFKVAIVITDGOSQDD
VSEPSOLLRADAVMYYAIGYUNLWHHÖLHOMTGNPKVFTYUESFEOLDARLADSLTM
SMCKTEFRPGTPEIICGPDRIGVKASTKQPFEGNVFVMDHYHDEECRAGPEKFPDSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(8540. .8572,9335. .9416,9468. .9679,10373. .10721,
10772. .10974,11033. .11175,11871. .12501)
//gene="M142.2"
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10772. .109
  /translation="mQSFDIESLIGVNKVPSIVEMVAASRASSFSPPFEQQHHDPMGV
VAAAAAAAAGRHHPYDNRDDGQMRRYRTAFSREQIGRLEREFAKENYVSRKTRGELA
AELNLPEGTIKVWFQNRRMKDKRQRVGGLAWPFPPQMAAYMLNPFAYEMMKTAAASQ
                                                                                                                                                                     E-value=7.1e-30, N=1"
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                                                                                                    /protein_id="CAA97809.1"
/db_xref="GI:3878738"
                                                                                                                                                                                                                                                                                                                                                                                                                 ADRPVLQFQCQITLCLKYDGGCEGITPPQNCKKLPGEDGHHHHHHPEKRRKLVRRLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q21540"
/db_xref="SPTREMBL:Q21540"
/translation="MRPIPYDISLSITSFLSLILICSANPIDNGLYDSELIHECYTHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA97806.1"
/db_xref="GI:3878735"
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/db_xref="GI:3878736"
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/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGLTVPFSACNVHRYRSLNPKGIFVEVSIVFMFHSLFMTKTDQTVKVQCFYMEADKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=]
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                                                                           db_xref="SWISS-PROT:Q93899"
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                                                                                                                                                                                                                                                                          22840. .23053)
                                                                                                                                                                                                                                                                                                oin(17427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="III"
                                                                                                                                                                                                 pte="VAB-7 even-skipped homologue, contains similarity
Pfam domain: PF00046 (Homeobox domain), Score=111.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is NOT necessarily the entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST yk258al.5 comes from this gene EST yk532all.3 comes from this gene EST yk532all.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA EST yk258al.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                   23053
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10974,11033. .11175,11871. .12501)
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                                               ORIGIN
                                                                           BASE COUNT
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CDNA
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CDNA
                                                                           QQVDMELQQLHLNPTVEG"
6626 c 6322 g
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/db_xref="GI:3878737"
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cDNA EST EMBL:T01774 comes from t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGATGPGNGAYGNNGSSTSPSAAGSLPFLPPLGFPSFLSQNSTKSPSSPHSDDSSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:045962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:3878739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA97810.1"
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  5.4%;
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  Score 62.6;
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  BG
  ω
Length 36306;
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JOIN(34039. 34101,34448. 34750,35530. 36306,

299276.1:105. 6.98,299276.1:1364. .1566,299276.1:1666. .1772,

299276.1:2495. 2795,299276.1:3714. 3928,

299276.1:4056. .4104,299276.1:3714. 5958,

299276.1:6478. .6729,299276.1:7169. .7338)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(34039. .34101,34448. .34750,35530. .36306,

299276.1:105. .698,Z99276.1:1364. .1566,Z99276.1:1666.

299276.1:2495. .2795,Z99276.1:3714. .3928,

299276.1:4056. .4104,Z99276.1:5846. .5958,

299276.1:6478. .6729,Z99276.1:7169. .7338)
                                                                                                                                                                                                            QSPTHLPGGPVVMIPQQQMVPPPQSMTPVGGPMGPMGPMTPSIPVQVPPNTMWTATSP
TGSVIYPAASPPGQPPHTIWIQSIGVFKRKSNFLKIVRKISFFLNFYDFFLILRKLKK
EKKGADIEFFEKIKSTDFKKYPSSFSRTDGNMFPMFDRGSGGMVWGPGTMLRESGADA
                                                                                                                                                                                                                                                                                                                                     LAGSQTSMLVPAXRYELTQVIPCLEFFAGIEHEDTSMRMIGDALHQIRILLKLHCSQD
DLRKWFEERRGVILQAEVPGOMGGGPGSGGAEARIGGLHPLYSQIDETGRSISRT
NPKONSHNSPQTFPKQPRQKRYQMGIPPNRMGYSSDAPPFISHQQQPPDGFYSQHL
PQRFRGGRQRGAPPPPPPPDPMLIGYDMPGAPMMQATEVLTADGQMVNGTPQRVVIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIEIILSIQSNTHYSSQLWSAVRARGCQFLGPAMQDDVLRLILMTLETGECIARKNLY
MYVVQTLASDYPQVSKTCVGHVVQLLYRASCFNVLKRDGESSLMQLKEEFRTYESLRR
EHDSQIVQIAFESGLRIGPDQWSALLYADQSHRSHMQSIIDKLQSKNSYQQGVEELRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mapTGQGGQWQEVLCCSICNRHFNETFLPVSLICGHVICRKCAEKPENQTKPCPHDDWKTTHSPSEYPNNVALLSVIFPRKQCWTLSGAVSEAEKRVDQLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKEMAINKPMIRIFNSEHLKNIKVLSEALEESEKFARAKTEQFAQNNPVNGTRTTERL
DKTLGELTPNLMKSPAISIRQQQXILQUKRTILPTCWCGEDIRVLGLVLLVHKPYEVSD
VTKDAKATGFDESRAESAVLQVQKILSKPMTEVTARAPLDFTIGAIVANYSSSEMSDT
DDIPQLSADTLAALSMFQAEQQEKIEQLOGGIIEKIDEDWQLSQFWYDDETSRKLVAE
                                            PVIPMVQVPVQVPIVPAENFNPNVPPPPPPPPQGQPMLVDSAIGLLTPIRPILVAHPQN
                                                                                                                            EQLLAKRYEILKRLQPSEDDDDPEDGGIGHVSYTVASSVLDDRMDHHPLTMIPVPTID
LPAIPISFANMPTEETMTMIGEMVQNRPRAPSLTAPSSNQPMNVNASASATVQAECEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIAKFFREADSERGGTVSSREISRTLQRKVLALLCYQWREVDGRLKTLKMCRGISERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Zinc finger, C3HC4 type (RING finger)
cDNA EST yk49h8.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVAAALEGSEARPARIGCVSSPTLVKFFHETEEYKTGQIQLTLFEFDDRFGLKFPTEF
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join(28250. .28366,28422. .28499,28558. .28991,30672.

31500. .31763.3233. .33043)

/gene="M142.5"
VVSNSLDKIVDVKERISEAQGNASEAENAHLRMELRMAESQMAHLDPYTKNNCLLRAI
                                                                                         RKILDFPLKYRKMTLMFEKVSTCFHVTLLKDYMVFYVLNTLNFASRWPRRRRAATIPQ
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/translation="MASCNLTASNVAIGACVEIETTNGLSARGVVISFDTTRKVLVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA EST yk470a9.3 comes from this gene NA EST yk470a9.5 comes from this gene NA EST yk4656.5 comes from this gene NA EST yk653c12.3 comes from this gene NA EST yk652c9.3 comes from this gene NA EST yk679e8.3 comes from this gene NA EST yk679e8.3 comes from this gene NA EST yk53c12.5 comes from this gene NA EST yk53c2c9.5 comes from this gene NA EST yk662c9.5 comes from this gene NA EST yk679e8.5 comes from this gene NA EST yk679e8.5 comes from this gene
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analysis //sequence?

sequence for a sma insert of

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ACCESSION
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196; Conserv
                                                                                                                                                                                                                                                                                                                                Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                       neighbouring submissions. The true left end of clone ZK265 is at 1 in this sequence. The true right end of clone ZK265 is at 2412 in
                                                                                                                                                    sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone ZK265.
                                                                                                                                                                                                                                                                                available information.
Current sequence finishing criteria for the C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortius Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                    It may be shorter because we only sequence overlapping once, or longer because we arrange for a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEZK265 36069 bp DNA linear INV
Caenorhabditis elegans cosmid ZK265, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dobson,R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.elegans Sequencing (bases 1 to 36069)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 275713.

For a graphical representation of this sequence and its see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/name=ZK265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The true left end of clone T01G9 is at 35964 in this sequence. The true right end of clone T02E1 is at 4168 in this sequence. The start of this sequence (1. .110) overlaps with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlapping sections once, or longer because we arrange overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The end of this sequence (35964. .36069) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z81581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT:
                                                                    /note-"predicted using Genefinder contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score-59.9, E-value-1.7e-14, N=3; PF01484 (Nematode cuticle collagen n-terminal domain), Score-74.9, E-value-5.6e-19, N=1
                       cDNA EST yk65d1.5 comes cDNA EST yk65d1.3 comes
                                                                                                                                                                                                                                                                                                                                                                                /translation="MPVAKEDSWAFQDIGSPFPEAPVRVPNQNNQVALWYKHGKPIH
GRAWNNDGVVECSFFYNKAELKGKLDLGGQIQILGYKGDYNSEGAFANEWI
NEGIREIVRCGSFFYNKAELKGKLDLGGLQIQILGYKGENAGTTEKKEGGAFANEWI
IFRNLRPPFTGLKVYDDLWYDLRYGDNFPSNAVPADGRALWTETGPHMQYVALWYKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KHDYNIKKRVTVGGHTIGADVFKLPNFSFEPSKVSTLEDMIHDYFKRTGNIIRRSVRI
PLHDDLHQPSSSTKPFVGHVPGLSLVCVPVFNKESVEYANSKZENLQKWYNLCHKQPE
MFDIHTKNMILLLERWLIDSQTFDSYFLSHFFMKESSRTRIKTCVHNPAFIDLQEQCI
RHMSHSVRSNVSSASADLDDRVHVANIAKIAMLRYNKFTISVINPAFNPHFASEDSSC
VYFYPGIKQCRAVACRAASSTSQDMRSRLYFLHKAAAEDGNAEEIRRELKIGMDSNLRDDD
                                                                                                                                                                                                                                 /gene="ZK265.
complement(jo
                                                                                                                                                                                                                                                           complement(join(6676.
/gene="ZK265.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWTPLHYACTHGHLEYVHELLNSPOMTA INAONKGGATALOZAVINGRBYLVEILTSH
ASIDVNIQNNEGYRPIDYCGNHPAIQKILELQIFKKKINVDDTSIGSFSIKSTSPEEAT
VGEVLDRLAEETQLNREQMNCTALFVYSESMSLQLQEDSILIDGKLKVDKWNTTIKKLV
GLIPPETPRLKLKRNAYATARMEIVTYSIEAVIFINIEDIKKRNQRSYYSDQHY"
                                                                                                                                                                                              comprement(join(6676. .7754,7804. .7870))
//gene="ZK265.2"
                                                                                                                                                                                                                                                                                                                                   SSGWTTVHIGNSAPCILKDDKGLEVLGNLDLTIEKASAGYGGKEKIMTGAAVAKLKVL
                                                                                                                                                                                                                                                                                                                                                          DPVFGRSYPSSAGKTMAHFGKNNQENAGPEVGSMQLLTVPEASCMGLEYKWMPLSEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB03515.1"
/db_xref="GI:3881551"
/db_xref="SPTREMBL:Q94401"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(5062. .5393,5442.
/gene="ZK265.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"predicted using Genefinder
Similarity to Human G9A protein (TR:G287865), contains
similarity to Pfam domain: PF0023 (Ank repeat),
Score-63.6, E-value-1.4e-15, N-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ZK265.1"
complement(join(492. .736,782. .932,983. .1189,1629. .1758,
1943. .2076,2124. .2289,2385. .2762,3174. .3313,3365. .3446,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(5062. .5393,5442.
/gene="ZK265.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MAEVSVAIVRLKISALSDKAIPSAQDFEICVKEEPSTAKNFGPV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB03514.1"
/db_xref="GI:3881550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q94400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ZK265.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="2K265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:6239"
/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is NOT necessarily the entire led clone. It may be shorter because we only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .36069
                          comes from this
                                                                                                                                                                                                                                                                              .7754,7804. .7870))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5628,5925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5628,5925.
                                             from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6428)
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gene

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/db_xref="Sptremb::Q94403"
/translation="MINATE:EIRED.HADDLTVMAMFIRNSHOMPSSIGVLYQAVLF
/IFETTLYCKYTAMETOKFIK.YOKLFYTRIFHNORNIFISLLLLWFELLYCRV
LLWAFKYNLAIEIRESIKCNDECHHFGRCSVAKNMFDSIFIAANMRYHYMYFVITPV
GLITERIFATILVKDYEKKSHWIFGLLFVAQNIFSCTMAVVTTTSGLTFQVLISGVI
FSLFCSAVVIALVEYFNOQRLMTLERDHRTTNYTLSIRVQLKENLKTILKVMRRFFISI
ILIILAMGLMSLFVILMLNEDIILTVRVYMDYVFHSMPVFLVFTAIFTIENTRKYTF
IKARTTFGMRIDSRKDEMEKLDELDSRFPSIIMSTRRSTRADSTTKRPASPNSTP
NAALGIFVAIAROLLEIDARKVALFYLAFVTULSFIESTIELDSTYYLVQKHSVLNQY
GVKMGMFWTLVIVGPFIWFSSKAHNREDRDQFIVDVCRLGVGTACWYTSVQFHKVLA
LTSMCDEMETDEVGGCEKECVWTPGYDISGIGFFMIYSILITEEAIAYRHYQQVTD
GVKMGCKFTLTRAQCSEKECVWTPGYDISGIGFFMIYSILITEEAIAYRHYQQVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(16560..16667,16744..16929,16977..1713:17179..17280,17420..17619,17656..17765,17814..17848,18123..18173,19898..20006,20052..20188,20236..20358,20406..20562,20879..21047,21096..21217,21445..21489,21572..21710,21816..21861))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(16560..16667,16744..16929,16977..1713:17179..17280,17420..17619,17765..17765,17814..17948,18123..18173,19898..20006.20052..20188,20236..20358,20406..20562,20879..21047,21096..21217,21445..21489,21572...21710.1816..21861))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SWISS-PROT:094398"
/translation="MSNPTDNNSATSSITPNCEFLMFEVSTNLVIQFTYFVKLYDNYF
/TRANSFTGARPPPPLIEWNEXIKCESKAIIOLEPKLISFFESVSAFSSETTYKDSDS
FSSFESDSSPSKSSSRKNRDKIADKKORRNRTTFTTFQLHALEAAFDKTHYPDVYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity to Mouse homeobox protein S8 (TR:G51366), contains similarity to Pfam domain: PF00046 (Homeobox domain), Score=90.1, E-value=1.5e-23, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(8777. .8956,9538. .9646,9702.
9879. .9976,12270. .12598,13623. .13818))
/gene="ZKZ65.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MITSGQLYAGTAVALCGVAIVALTALAFAVLHDINSFOSGVYED
LAEFKILAEDAWITMVPREDAVQPFEIFLKRERGYGDAGVAGSASGSSGCNCGPQPK
DCPAGPPGPPGNPGTPEDDGPAGRAGNPGSDSTEGDRMADFNKDVKCPAGPPGPPGPN
GFPGHPGPDGDFGVDGTNGKDGEPGPDGPEGDDETDGPPGEDGPVGQNGTRGQGQ
                                                                                                                                                                                                                                                                                                                                                                                                     AVHQMDGDREEHDRLTRCIQYFFVAMLFLHAFWFKQIIISVLYYHIFIEEILGAVAAV
VCWFVTYRMLYPAGFLASPIRRTVGRK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA EST yk508e4.3 comes from this gene cDNA EST yk508e4.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPPQLTHSQENC"
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PPMLPPANTLSSTHNNGISDEFFKTSEGKEVYGFPFAEYGTPADNTHVSKTGNVFHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(8777. .8956,9538. .9646,9702. .9830, 9879. .9976,12270. .12598,13623. .13818))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGPVGAPGAPGGPGRDGEPGENGQDGQQGPEGPAGADGQPGHPGPDGPSGDVGEVGAP
GADAAYCPCPPRSAEMAATGSSDSQPASYEAPAPAATKGYDSPAPAAPKGYDAPAPTA
GAPDAPVAPPKLHDYESPAPVADAHDAADAAQPYKRKKARAHIV"
/translation="mardvkkrgkpaytnrrnrqxylkkkdnkkklsksavpiikytw
DETKTPRENVRDMGIAFNPNDAVPIAEHRKEIIDAEPIDGVSIVVPKPEKKVTGRKKN
                                                                                                         /protein_id="CAB03516.1"
/db_xref="GI:3881552"
                                                                                                                                                                                                                                                                                               /gene="ZK265.6"
/oin/1827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB03517.1"
/db_xref="GI:3881553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ZK265.5"
/note="CDNA EST yk481g5.5 comes from this
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/db_xref="GI:3881555"
                                                                                                                                                                                     /codon_start=1
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                                                                       db_xref="SWISS-PROT:Q94402"
                                                                                                                                                                                                                       'note≖"predicted using
                                                                                                                                                                                                                                                             /gene="ZK265.6"
                                                                                                                                                                                                                       Genefinder"
                                                                                                                                                                                                                                                                                               .18539,18656.
                                                                                                                                                                                                                                                                                                                                                                   .18539,18656.
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REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                COMMENT
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                             REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACCTGGATGCACATATTCAATT 35198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCACTAAAGTTGATCAAGCATATCATGTGAAATGCTTTTTTGAAGAAGCAAATAAGGGGC 35115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATCCACGTGGAATGTACTACGGTATCACAGTCGTCGTGTCTTTCCATCCCTTATTCA 35055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCAGTATGCCGTTATGAAATT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACTGCTGAGTTGGGTGTTAGTATGATTCCAACGACAGAATTAGAAGCGAGACATGGAA 35175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGA 448
                                                                                                                                                  Submitted (19-APR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; Carboxypeptidase b like;
Caenorhabditis elegans.
Caenorhabditis elegans
                                         sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones.
                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the nematode C. elegans: a investigating biology. The C. elegans Sequenci Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone WO1A8
                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                Wilkinson, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEW01A8
                                                                                                           Current sequence finishing criteria for the C. elegans genome
                                                                                                                                  available information
                                                                                                                                                                                                                                                                                                                                                       The C.elegans Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                       (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29467. .29631,29755. .29902,29982. .30024,30072. .30293,
30599. .30709,30782. .30854,30908. .30989,31418. .31619)
/gene="ZK265.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(27566. .27635,27677. .27835,28839. .28913,29226. .292467. .29631,29755. .29902,29982. .30024,30072. .30293,30599. .30709,30782. .30854,30908. .30989,31418. .31619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:1279337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ZK265.7"
join(27566. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKQAAHIISNLEQQVKEEEEARAGQDRKFRLFHRETELCVYMLARHGEDFQAMTRDPK
NLWQYTPKQWAKKIRTHKESEMCKFLETA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MRGTSILLPPNPATKMLEISRLPNFTRTSFLLIFPLHRFKAKEM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q94404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Nematoda; Chromadorea; Rhabditida; ea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%;
56.7%;
                                                                                                                                                                                                                                                                                                                                       25284)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.2; DB 3;
Pred. No. 0.00046;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25284 bp DNA lin cosmid W01A8, complete
                                                                                                                                                                                                                                                                                                                                                         Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuticulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 36069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .28913,29226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INV 24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 29303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .29303
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overlapping sections once, or longer because overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The true left end of clone F22D6 is at 25181 in this sequence. The true right end of clone F15C11 is at 12341 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence 271260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neighbouring submissions.
The true left end of clone W01A8 is at 1 in this sequence. The true right end of clone W01A8 is at 11258 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 271262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The end of this sequence (25181. .25284) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     name=W01A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 271262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [MPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                  LOW this gene CDNA EST yk163bl2.5 com/CDNA FC-
                                                                                                                comes from this gene cDNA EST yk383d9.5 comes from this yk417d8.5 comes from this
                                                                                                                                                                                                              yk281d10.5 comes from this gene cDNA EST yk302e2.5 comes from this gene; yk303e9.5 comes from this gene;
                                                                        cDNA EST yk426d4.
yk460c8.5 comes f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                      cDNA EST yk477f1.5
yk482d12.5 comes fr
                                                                                                                                                                                                                                                                  DNA EST yk303h10.5 comes from this gene; yk206b12.5 comes from this gene CDNA EST yk239h1.5 comes from this gene; yk281d10.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10206. .10307,10359. .10418,11007. .11117)
//gene-"W01A8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSTLDKFTPKGRKFVGCSTNCLVKAIVNISEYSTSCTQIQEEAFKSHVDCYLNCNFCE VCKTEKLAFLGSYDWTDFLSYAAVKQVLAIIRKCGIFSCLKVFDV"
join(9030. .9125,9180. .9776,9822. .9899,9955. .10158,
10206. .10307,10359. .10418,11007. .11117)
                                                                                                                                                                                               CDNA EST
                                                                                                                                                                                                                                                                                                                                                            cDNA EST yk442h5.5 comes from this gene; cDNA EST yk303h10.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MVKPKKEKIANKCVPTGEIVDKKAQESAIFSDTEGRIGLHIHAK
PGAKKSCVVAIGDSEVDVAIGAAPREGAANEELISYLMSALGLRKNELQFDKGAKSRS
KVVLLDTKALTIDELSVISAKPDPEICEKYEVVEQKFKCGPDGYPLHFGLRNCLMFNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
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/gene="W01A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA95853.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(5595. .5813,6012. .6100,6360. .64
7471. .7530,7729. .7856,7934. .8072,8122. .8142))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="W01A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(5595. .5813,607471. .7530,7729. .7856,7934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:6239"
/chromosome="I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="predicted using Genefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="W01A8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="W01A8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="SPTREMBL:Q23094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e-"predicted using Genefinder
EST yk75g3.3 comes from this gene; cDNA EST yk75g3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST yk275h2.3 comes from this gene EST yk309g11.3 comes from this gene EST yk275h2.5 comes from this gene EST yk309g11.5 comes from this gene"
                                                                                                                                                                                             yk339h11.5 comes
                                                                                                                                                                                        comes from this gene yk339h11.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                              /k163b12.5 comes from this gene; cDNA EST comes from this gene
                        comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It may be shorter because we only once, or longer because we arrange
                                                                        from this
                                                                                              .5 comes from this
                                            comes
  comes
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6,7934. .8072,8122. .8142))
                                            from this gene;
                                                                     gene
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this
                                                                                            gene;
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                                               CDNA
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                                                                                              EST
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19346. .19435,19
/gene="W01A8.3"
join(18064. .180
19346. .19435,19
                                                                                                                                                                                                                                                                                                    cDNA EST yk100d3.5 comes from this gene cDNA EST yk607d1.3 comes from this gene cDNA EST yk607d1.5 comes from this gene"
                                                                                                     /translation="MDPAMFRWYSADMTQAEFFRETPRTVFLYVGTVFALFYIYTRLM
FVPMDKSNEACLDGKLLWWDRQQGRTLQTGGSGLFAPTIGIDF"
join(21264 ...21365,21414 ...21568,21618 ...21843,21891 ...2208
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/translation="Mrimrcgspkvicaendlaldivtskpfrgnifvkgrakdksc
/translation="Mrimrcgspkvicaendlaldivtskpfrgnifvkgrakdksc
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CFYMEPDEIVTQNIDVSMIPTTELSDSMVMPKCEYSVRRDGPNGPTLTYANVGDIVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA EST yk615c12.5 comes from this gene; yk643h10.3 comes from this gene cDNA EST yk643h10.5 comes from this gene; yk670g10.5 comes from this gene cDNA EST yk679g8.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA EST yk540b10.5 comes from this gene; cDNA EST yk580a3.3 comes from this gene cDNA EST yk580a3.5 comes from this gene; cDNA EST yk5812a9.5 comes from this gene; cDNA EST yk612a9.5 comes from this gene;
                                                                                                                                                                                                                   /protein_id="CAA95851.1"
/db_xref="GI:3880397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(20058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (20058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHKKELDIMQSGRYY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWECTPADMGMLVKKCFVTDGDGEDHAVVDFDGCATDPFLLSELSYDASLMRAHASSQ
VFKYADSNQLYFTCQ1RLCQKQMGMCQEVTPPNCGVKKLLSEASGDGNRTKREADRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA95850.2"
/db_xref="GI:15718222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STIDYLENLKKNFTDAEDVYKVRDEVLNEGRQRIAELSTWTTSLLIISAEWQFEPEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EHRIFSALHQAQRIAMVPVEKITENTNSLLDILDGAVQKGLNIEVPPSVNLTIGQRVK
NLASLIVQGVSNKAHDHVIDPINERARNYLEQLSQSFVLLDIVREKKTWVIEKSNELS
TSVFDFKKTLEEEAQKYKVAPEEMLMKHIQSTSEQLSTQLQSLREKGQNVFGDGTKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTDVEQPVSVEDQQAQAQSYYDQVLGNAYVQTAINAYTKTKEFH
PLLNSTLNSAEEKVSTVGNYAAQKAYDGYNSYYVKPKNTAYEAVSYGTERAKTAVESG
KQAAIVGGTFGIGAAVVLTQFSLALSAGGAALVLEQVDSAKKLGSSAISTIKEAELAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA EST yk612e9.5 comes from this gene; cDNA EST yk615c12.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yk477fl.3 comes from this gene cDNA EST yk482dl2.3 comes from this gene; yk525fl0.5 comes from this gene
                       join(21264.
                                              /gene="W01A8
                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                         /gene="W01A8.4"
/note="cDNA EST yk100d3.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEIDVATSELLVLDPADRGLLAPSPFCVPRLLLPVLPLILITIVSLTVVSTALVIRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="W01A8.3"
/note="Similarity to C.elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA95854.1"
/db_xref="GI:3880400"
/db_xref="SPTREMBL:Q23095"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yk239h1.3 comes from this cDNA EST yk281d10.3 comes yk302e2.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA EST yk679g8.3 comes from this gene; cDNA EST yk239h1.3 comes from this gene
                                                                                                                                                                                            /db_xref="SPTREMBL:Q23098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="W01A8.4"
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19346. .19435,19506. .19721)
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22408)
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                             .21365,
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                          .21568,21618.
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                          .21843,21891.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19263 CAGAAACAA 19271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18972 CGTGATGGTCCAAATGGTCCAACTTTAACATATGCCAATGTCGGAGATATTGTATTTCAT 19031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 GATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCAT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 ATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTG 474
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                                                                                                                                                                      Caenorhabditis briggsae
Caenorhabditis briggsae
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Chromadorea; Caenorhabditis
                                       (bases 1 to 59533) Waterston, R.
Submitted (04-NOV-2000) Department of Genetics, Washington
                                                                                                                                      Rhabditoidea; Rhabditidae; Peloderinae;
1 (bases 1 to 59533)
Washington University Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis briggsae
                           Direct Submission
                                                                                            Unpublished
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FVDPLRTREHAIPEVASEVELINETKDNOPSTSSN"
complement(join(22578. 227756,22809. 22983,23343. 23481,
23564. 23757,24032. .24154,24283. .24565,25191. .25219))
/gene="W01A8.6"
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/translation="METDGDPTNEIPGSSMAFEVANHTVTEEPSPLDRILAEGRSFNG
GNWSSDDLRSLLDGVMKYGTKIEAINVIHRNIVKKRSIEEIKAKIDEIREIIKEHKEI
ILPECYKNKWIEAGHHNITPPPFCQVDDNDDWSSIMGKIVDHHGSINKTLPSLADTY
ETLFENLALESKTHENAVVTKLLTAKATRTDSQNIRWPYIYREMKACATLEEQMPALN
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/db_xref="GI:3880395"
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                          Direct Submission
Submitted (22-AUG-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
                                                                                                                                        Direct Submission Submitted (21-NOV-1995) Robert Waterston
                                                                                                                                                                                                      The sequence of C. elegans Unpublished (2001)
                                                                                                                                                                                                                                                                                                     Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Direct Submission
                                                                                                             Waterston,R.
                                                                                                                                                                          Waterston, R.
                                                                                                                                                                                                                                         Pauley, A.
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10893 c 11126 g
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/db_xref="taxon:6238"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 59533;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding sequences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of vojt Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFecome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-5E (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The 5' cosmid is T02G5, 200 bp overlap; the 3' cosmid is T07F8, 1000 bp overlap. Actual start of this cosmid is at base position 1 of F10E7; actual end is at 7817 of T07F8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-MAY-2002) Department of University, Genome Sequencing Center, Louis, MO 63110, USA submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-SEP-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.wormbase.org/db/seq/sequence?name=F10E7;class=Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             graphical representation of this cosmid sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
/note="coded for by the following C. elegans cDNAs:
yk44g1.3, yk20f8.3, yk12b7.3, yk12b7.5, yk16g12.3,
yk16g12.5, yk20f8.5, yk36g6.3, yk36g6.5, yk44g1.5,
                                                                                                        complement(join(900. .1126,1176. .1637,1685. .1769, 1985. .3460,3510. .3689,3736. .3885,4119. .4291,4518. /gene="F10E7.8"
                                                                                                                                                                                                                                          complement(900. .4554)
/gene="F10E7.8"
/note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=F10E7.8;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis
/strain="Bristol N2"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                          /clone="F10E7"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEIGHBORING COSMID INFORMATION
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4444 Forest Park Avenue,
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IVERCOIKSGGIYFLVSHVLGHOIGGAIGIIYAFGQAVATGLVAVGFGESVAHLFESE
SKIMIKGIALLTLMVLFAVNTAGVTWVVRLQIVLLTIALAVTDFIFCALFSSBPESG
VFRESSERIRVNADSHYEAVNGSIIGIPROIPEGSFETVFGVFFANFLGVLAGVNMS
DLKDPHKSIPLGELSAVGVSSTICFIFIMILGGVGDRMFLLCDVMISEKVALTGIVFL
VGLYVCSLSSTVGPNDNPVLAGYLLMGVASLEVLLGDLNQLAILGTWFFLTYAYVNY
SYVSLAMSYLLATVQHADEVETYGVGSTNKMNDLNELFPERBDVNITSTEFTETTGIS
GEATWYSMFSNRYVSFLGFLVNLAIILLLIFWFAVAHFVALIALYWYIGRVCPTCGPG
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/protein_id="AAA83423.1"
/db_xref="GI-1086832"
/translation="MSETGPSSSHSVVVEPPDSIFSQGETADSSQLPWWQRTILTKDK
VLFGTWDGVFATVMVNIFGIIVFLRLGWIYGTAGVANSILLLGICTSLALITVFSAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=F10E7.9;class=Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Ribosomal_L35Ae), Score=256.8, E-value=9.6e-74, N=1; coded for by the following C. elegans cDNAs: yk51f3.5, yk64g10.3, yk99d1.3, yk1567.5, yk1567.5, yk1577.5, yk207c1.3, yk207c1.5, yk221f10.3, yk229g1.3, yk229g1.5, yk282e4.3, yk282e4.5, yk298e8.5, yk308e6.5, yk402a7.3, yk438g5.3, yk438g5.5, yk449b9.3, yk449b9.5, yk450d5.3, yk450d5.5, yk460f8.5, yk467g1.5, yk468d11.3, yk480c10.5, yk468d11.5, yk480c10.5, yk462f6.3, yk482f6.5, yk64g10.5
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EVQEPT ENGNEPLLIVLFDMLHPFYIGTAPHFPIKKIVLLIVLLLTRLGGWEELTVR
KREKRMTAGLDIMEDT ITVAASQAAFIAKDQEHVRNMAHRAGSFARGMMARQMAYND
DSKDEDAYSEASSEDSTIASKKEDSPEQASSSTPSIEDTASNFRQGSGEDTBPVGSPP
FPVIQKKTLPWRSKTNAQDIEDFIQKGRFKYFNYDFDPGDDTTLFGLPPSFCGAVKIL
RNNMYTSLTELQVKKDELNRYLFSMKEDIPETKTETLYRKILPMLSQYICALVKVMV
SSVPSTKARHEGLNVLIDCLTPEMEASDILSNSISLDNSTSSPLEGFFKAIDINRK
EIIVKSLSAILLLLVKHFKLNHIYQFEYICQQIVYVNGIPLILKFLDQNTNKLIQSRH
EIYAYNYPQCLYHYVRNNEEMFILTQDNIEEPRPPGAGPYFMWRNVFFAINLIRLLRLNK
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sequence F10E7.7)"
/protein_id="AAA82422.1"
/db_xref="GI:1086831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(5858. .5968,6012. .6221,6265. 6769. .7271,7551. .7752,7801. .8020,9268. .93
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/gene="F10E7.9"
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GVFNKEDAGFYAGKRVVYLYKAHNKTLKTGHTVATRTRAIWGKITRPHGNAGAVRAKF
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4936. .5624
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/product="C. e
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/gene="rpl-33"
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ISAIYSRVRHRMTDDWAFASDIKRKCDYQKEDSLIKASIERFHSRRYSALYPQFAIEV
ISTESLCHMEKTVESSLDSLRSGATTILPETTETSGVSSSQQNEANPDYQDRRQYHHS
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ADLEVRLKSARIILFLLQGSATDFGCLENEEIEYQYDQKLLMNVPIRKTKEMDPEGPS
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/protein_id="AAA82421.1"
/db_xref="G1:1086830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="coded for by the following C. elegans cDNAs:
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MEDLINE
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                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                       ORGANISM
           TITLE
                                                                                        REMARK
                                  AUTHORS
                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14488 ATGCCAAAGTGTAATTACTTCGATAAGAAAACAAGGAAAAGATGGTCCACCAGTACAGTAT 14429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14377 AACGGGATTCTAGTACAGAATTGCCATGTGGAAGATGGACAGGGAAATAAGATTCTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 TTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGGTAACGGTGATACTGTGGAAATT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 ATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 TTCTATCAATGCCAGATCAGTATTACCATTAAAG 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 GCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAAACCGTTGATACT 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTTTTATCTGTCAAATCAAGATTTGTATGAAAG 14164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAACAATCGATTGCATTTCAAGAAACTCATGTGTTCAAATTTGCTCAAAGAACAGTAACA 14198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTCAATTGGAGACAGTGTATTCCATGTTTGGAGTTGTGAT-----GGAAATCAT
                                                                                                                                                                                                                                                                        Caenorhabditis elėgans.
Caenorhabditis elėgans.
Caenorhabditis elėgans
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                          HTG; Casein kinase I; Cuticulin; SH3 domain; Transposon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEM28
                               Gardner, A.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z49911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans cosmid
                                                                                                                 99069613
                                                                                                                                                                                                                                 none
                                                           (bases
                                                                                     C.elegans Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MARSRRDKNVSLTKVKKKTKDTKNNLVNEVRASVDQYKNLFIFT IANKSSTRF 1AIRQKYKENSRFFFGKNNVISIALGKQKSDEYARQLKKASAILKGQCG LANKSSTRF 1AIRQKYKENSRFFFGKNNVISIALGKQKSDEYARQLKKASAILKGQCG LANKSSTRF 1AIRQKYKENSEEDVARVGDVATFTVVLPEBFDISQFAFSNEPDLRKUFLF LANFNMSKKEVEAEFSVERSEEDVARVGDVAKILKHFEVKMSQFRLIFKAHWNKKDGFKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to 60S acidic ribosomal protein Po (L10);
coded for by the following C. elegans cDNAs: CEESI89F,
CEESR40F, CEESN26F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(11359. .11386,11435. .11493,11541. .11618,11668. .11846,
11894. .12212)
/gene="F10E7.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="for a graphical representation of this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Hypothetical protein F10E7.5"
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/db_xref="GI:1086833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=F10E7.5;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12451. .12959
/gene="F10E7.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:872077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                           to 40265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54.8; DB Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40265 bp
                                                                                        Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    м28,
                                                                                                                                                                                                                                                                                                                                                                                                                       Esterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28396;
                                                                                                                                                                                                                                                                                                                                                                                                                       L7AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the specified clone. It may be shorter because we only overlapping sections once, or longer because we arrange overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone M28. Important because we only sequence overlapping sections once or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUN-1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neighbouring submissions.

The true left end of clone M28 is at 1 in this sequence. The true left end of clone D2089 is at 40166 in this sequence. The true left end of clone C1089 is at 5382 in this sequence. The start of this sequence (1.101) overlaps with the end of sequence Z49909. The end of this sequence (40166. 40265) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics, Washington University, St. Louis, jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                available information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence Z36948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPORTANT: This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                  join(2766.
4867. .500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(Z49909.1:38615. .38695,Z49909.1:38912. .39184,
Z49909.1:39393. .39575,Z49909.1:39631. .39784,102. .242,
292. .412,462. .924)
/gene="C14A4.13"
join(Z49909.1:38615. .38695,Z49909.1:38912. .39184,
Z49909.1:3933. .39575,Z49909.1:39631. .39784,102. .242,
cDNA EST yk389e11.5 comes from this gene cDNA EST yk5120a3.3 comes from this gene cDNA EST yk512f1.3 comes from this gene cDNA EST yk647d10.3 comes from this gene cDNA EST yk659c11.3 comes from this gene cDNA EST yk664a5.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains similarity (Eukaryotic protein kinase E-value=1.2e-09, N=1"
                                                                                                                                                                                                                                                                                          Join(2766. .2816,3520. .3577,3647. .4214,4456. .4603,
4867. .5009,5322. .5712,5991. .6251,6448. .6547,6672.
/gene="M28.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEEEKLVYVLDFGLCRNMFNKQKELRKPRMKAPFRGTILYCSLNIHQRMEPGRHDDFW
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PDYVKLREVLCQIMTSKKFTPDMPLDWQKGGPCEAIFKPQAAVVKHKGTKKKVSLAEL
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RRNSPNTRFACKAELAIDHNNLKTEWDLMTLLKDNKSKHNIIGVELGSERNFNYIVMH
                                                                                                                                                                     cDNA EST EMBL: T00366 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                 GVTMSLKPQLAQQRCSAEHKDLSTPPAIARSPIGQNTTMKPPVTAIPRPPIEKHSVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGPSLSDLRKTVPNKTFTLFTTAVCAIQCFDSLVEIQRIGYIHRDVKPSNFAIGVLG
                                                                                                                                                                                              /note="similar to cuticulin
                                                                                                                                                                                                                        /gene="M28
                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLPKPGGKVYTERDFPQPGEQEPMRDESVSKSDDTIIEKEGPPPAPKPVSKPVPPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA90134.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="C14A4.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="M28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ∕organism="Caenorhabditis elegans'
                                                                                                                                                                                                                                               .766. .2816,3520. .3577,3647. .4214,4456. .4603,
.5009,5322. .5712,5991. .6251,6448. .6547,6672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to Pfam domain: PF00069 domain), Score=36.9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
for a sma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    once,
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//dl_xref="St-30,0000

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PDIAETFLLPRKNETTSDTDEGEWKGIGGASAGGNAIFGGTRGEERLVFCKSVTSSST
RSRPGSTLPLGTSSSPDCPFLTTCAPCACEERTRRATNSIRLEVPLNSCNTKEDRKL
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VIDQHGCTLDQLMLQTPTYSEDGMSAQVDAYIFKFDDRSTVDFROTITFCSVDDAECL
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TFEEYERTFCVSVASFGILISASTFFATISIAVQFLLVSRFGCYQTEKLAEKSTMTPL
CMDVCYGETTOKTV
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GSTGFYGVGKGISDGLQKAPDSQTYQDLNNLISGKESYADTIKSMVLSQVGAIIFWSV
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NLAETDLTDSIDNGVTYADKIVTDIFDVLSNGKNQLTCEVKSSTSQALAEIRSFIKNY
{	t AEDVIDGTTTRVGLTAVNNEDSDAFKRSTEVTYNKGVKLIGDLQTLQMSPKTGPDCRN}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(13937. .14329,14377. .14533,14662. .14822,14873. .1
15203. .15286,15367. .15528,15577. .15697,15742. .15953,
18567. .18749,18794. .18874,18928. .19155,19478. .19573)
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                                                                                                                                                                                                                                                                                             db_xref="SPTREMBL:Q21572"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="M28.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMRYSYFEIRKILYSKILSSPEVGONAVTEEVTVEFCLYTKIOSKQNCTQSVELFLN
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Join(8730. .8930,9116. .9304,9425. .9581,9781. .9941,

10191. .10349,10393. .10476,10521. .10679,10729. .10852,

10901. .11120,11492. .11672,11713. .11895,11940. .12020,

12065. .12289,12604. .12677,12964. .13056,13233. .13358,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA EST yk510a3.5 comes from this gene cDNA EST yk512f1.5 comes from this gene cDNA EST yk647d10.5 comes from this gene cDNA EST yk659c11.5 comes from this gene cDNA EST yk659c11.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA90132.1"
/db_xref="GI:3878696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="M28.8"
/note="cDNA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(8730: .8930,9116. .9304,9425. .9581,9781 .9941,
10191. .10349,10393. .10476,10521. .10679,10729. .10852,
10901. .11120,11492. .11672,11713. .11895,11940. .12020,
12065. .12289,12604. .12677,12964. .13056,13233. .13358,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="M28.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA90131.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=]
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EST yk288h7.3 comes from this gene
EST yk321g1.5 comes from this gene
EST yk288h7.5 comes from this gene"
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REFERENCE
AUTHORS
                                                                                                KEYWORDS
SOURCE
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ACCESSION
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                                                                                                                                                                                                                          CEW06D12/c
                                                                               ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5385 TGATCAGAATGGAAACTCTGTTCAAAACAGTCTTGTTGGAGAACTGGTTCGACATCAATG 5444
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                                                                                                                                                                                                                                                                                                                                                  717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 TGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATG 539
                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                                                                   GATGCTTCAAACACCAACATATTCTGAAGATGGAATGAGTGCACAAGTTGATGCATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGA 599
                                                                                                                                                                                                                                                                                                                                           ATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATT 768
                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCTGTAAAGGAGGTTTAACTAATAAACTAAAAATGTTGGTGCATCAATGTTATGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150;
                                               Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                       HTG.
                                                                                                                                                          Gaenorhabditis elegans cosmid W06D12, 282073
                                  Rhabditoidea; Rhabditidae; Peloderinae;
                                                                                                                                        Z82073.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA EST yk59911.5 comes from this gene cDNA EST yk59911.3 comes from this gene cDNA EST yk286e3.3 comes from this gene cDNA EST yk286e3.3 comes from this gene cDNA EST yk286e3.5 comes from this gene cDNA EST yk285a5.3 comes from this gene cDNA EST yk225a5.5 comes from this gene cDNA EST yk205a5.5 comes from this gene cDNA EST yk200c5.3 comes from this gene cDNA EST yk200c5.5 comes from this gene
                                                                                                                                        GI:2653149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFWSVGIVLIIIAAALCIVTCIWQCCSTCAPRESAVRSEYTGMVYLALLATTLAFTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKLRLFVGFIALISIAFCAKSPKPQASGPAPAQCPKSSVEVKPM
KPELTGSVGFYGTGKGISDSLQKTPDSKSYEDLNNLISGKESYGETLKSMILSQVTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(20244. .20468, 20516. .20698, 20746. .20902, 21009. .2:
21220. .21378, 21607. .21690, 21739. .21897, 21948. .22068,
22115. .2237, 22457. .22643, 22712. .22894, 22941. .23021,
23067. .23285, 23437. .23531, 23579. .23791, 23862. .23997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:Q21571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA90129.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="M28.9"
/note="cDNA EST ykl34ell.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQAVTKLFKALQDDIFKCRPLVDVYNNAGISVCEQFGLPVHGMWASVGLGGVVLFFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNNLDQTF TAYSESLSMSHLLSQQFVKKLETLAENAPKTPSTAKDLNKTYFTKTEATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAEVSLDDTINSIVHFLDKLQQEVKAVKKISIPSIHQKVVSYVSTGMVIGIRVGVTIL
ACLGLICCILAIVVVVLSLMKQDGLAMKLSVAVIISFFVSIVLCIILFKIAMTVFAMG
LVVSSVCVPVFGDDKYTLLYWNSDSSNWKSFLNQHWIAKKLLNDNAEQAKSANLAICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="M28.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            )oin(20244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILLLLTFRWLRTHSKNTVGKNGKSDKTGTSGSMEKAGSKEKDKKKKKKKKDKANPTDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%;
51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53.6; DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.04
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                DNA
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                                                                                                                                                                           complete sequence
                                    Caenorhabditis
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                                                                                                                                                                                                  linear
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REFERENCE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neighbouring submissions.

The true left end of clone W06D12 is at 553 in sequence ALO23857.

The true right end of clone W06D12 is at 2303 in sequence Z93782.

The start of this sequence (1. .104) overlaps with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-NOV-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 ISA, England and Department Genetics, Washington University, St. Louis, Mo 63110, USA. E-ma jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 29, 1997 this sequence version replaced gi.1695114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. It mookrant: This sequence is not the entire linear tof clone W06D12. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=W06D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the specified clone. It may be shorter because we only overlapping sections once, or longer because we arrange overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The end of this sequence (34265. .34368) overlaps with the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basham, V.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The C.elegans Sequencing (bases 1 to 34368)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence Z93782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence AL023857
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NLKWFLSFHITAITCQWLCSFLLIDFYTFVPSKITRIDGLLIDFIDAKVILYTSKYILS
ALSTSSCLLLFCNSVENIFNMLRNNKSWLRTFSEWLAWTFVLMFPFMSLLGFFIRDQP
                                                                                                                                                                                                                                                                                                                    join(2263. .2429
/gene="W06D12.7"
                                                                                                                                                                                                                                                                                                                                                                             AKCRRPPVSHSDVMKPFVTENYWWFDNYMIQRPQITCFEK"
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/db_xref="SPTREMBL:045895"
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                                                                                                                                                                                                                                                                                         join(2263
                                                                                                                                                                                                                                                                                                                                                                                                     PDTFTMAGVVCAKGQWHLNGFALFVEPKFSSITRHCNCDPVSQVFTYQFHSPTNQHFT
RAIDREDVYINRTIEGGTRKNIVESCEFTYTCAGDGDLVVFSWENGPIPVRFPGQTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(1055. .1180,1224. .1326,1402. .1631,1673. .1816)
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/gene="W06D12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                  .2429,3400. .3736,4267.
                                                                                                                                                                                                                                                                                         .2429,3400. .3736,4267.
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                                                                                                                                                                                                                                                                                                                                                  .4764)
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for a sma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a small
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CDS
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IGLGDIMPNNATVGNNRNIYENEKIKFAPIISIIFFFGMAVTKVVNRNTFIAVENGIF
GAFTLVENKLDAIVTRSSASVKPEDRPSTPKVQRALSVDAGSEVQDETPNEILNNLTV
RSIATFMKSNADIYGGGFGRVQLRRGDLIHSDSQNQMTVNSMSQLRHRTASQSQPNQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(5022. .5258,5402. .5535,5584. .5957,
6431. .6584,6629. .6770,6823. .6945,7344. .7618,7718.
8766. .8883,9010. .9145,9196. .9207))
/gene="W06D12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(5022. .5258,5402. .5535,5584. .5957,
6431. .6584,6629. .6770,6823. .6945,7344. .7618,7718.
8766. .8883,9010. .9145,9196. .9207))
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                                                                                                                                                                                          VVILVLLYTLLGAVMFWTVESRHEKAKTLDHVNNLEHLLDRLAENITESVNNINTTTT
EEEMKVYIRBAYIELMKLEGOYKGSTYKLEADDNMKWFFESAAFFSMNYYTTTGOGS
EEEMENYIRDAYELVCVYGFIFFVPVTLVLRDLGGFEVHLTKLYAHGIQKFRELNGAKHV
DEDEIISLPIKACLLLLASYLGACTIFIYFYDELSGPEPGTGMDMFLCFYFSFISLST
                                                                                                                                                                                                                                                                                                                                                     SHSENDFKRKNAIRSEETPEISPEIQRIEDPLASSDEEENEKPFARSISVSNADLEER
HRLDSIPENDRSQQSRYTRHSSIDKGILKPQNNSEDVVEKYYERNNYTVTGRDRPDFY
NKLPGRLQHRLSVHTDAASRFSSPGAMGEPVVPTLRRFDKSMYWFAFHRKQIGFRHFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="cDNA EST yk224a2.3 comes from this gene cDNA EST yk224a2.5 comes from this gene"
                                                TGGNNNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB04926.1"
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    )oin(13888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:045894"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MTSEQQNNYYPRGNVPRHSAVLEEIHEEEQDSIPEEDETNLEKP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
14185,14708. .14777,14968.
    .15102,15147.
```

/gene="W06D12 )oin(13888. 14185,14708. .14777,14968. .15102,15147. .15423

/note="contains similarity to Pfam domain: PF01461 (7TM chemoreceptor), Score=-36.9, E-value=5.1e-13, N=1" /gene="W06D12.4" /codon\_start=1

/protein\_id="CAB04925.1" /db\_xref="GI:3880549"

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GFFLAVIFAVHFIFRYWTITKNDKIRFFNFPYFICWIIGSYYFGVEYSYILHVEFSER DISSTSRALAQVAGNQVAPAVVIN" PDKTEFIRQKMSEDFGHTMDEITYMAARFVKYSEEAGALTIDWRQVGFYFAATKTMIL

join(19946. join(19946. /gene="W06D12 .20159,20215. 20159,20215. .20551,21208. .20551,21208. .21658) .21658)

acid cDNA cDNA CDNA /note="contains similarity to Pfam domain: PF01069 (Fatty /gene="W06D12.3" desaturase), Score=465.8, E-value=1 EST yk4148b12.5 comes from this gene EST yk412h2.3 comes from this gene EST yk412h2.5 comes from this gene EST yk42h2.5 comes from this gene EST yk548c4.3 comes from this gene E-value=1.1e-136, N=1

CDNA /codon EST yk548c4.5 comes EST yk661f6.5 comes

CDNA CDNA

from this gene from this gene

CDNA

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RESULT 31
CEF20D1/c
                            DEFINITION
                                                        FOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30469 AGATGGTCCTGCGACGGCAACAACAAGAATGTACTGCATGACTGTTCACTCATGTGTA 30410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30409
                                                                                                                                                                                                                                                                                                                                                                                                           30349 GCGTTCATTCTGAAAGAGTTGGAGTATAATGAGAAAGAGCTGGAAGCTGGGCAAATGTCA 30290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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                                                                                                                                                                                                                                                  772 ATTAAAGA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 AAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTT 594
                                                                                                                                                                                                                                                                                                                                                  712 CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 AAATATTTGCTAAATAATTTGGAATATCCA---ACAGATTTAATGGCTGGCCAAGAAGCT 711
                                                                                                                                                                                           ATGAAGGA 30222
                                                                                                                                                                                                                                                                                               AGTGTTTTCAAGTTTGCGGACAAGCCGACGGTTTTCTTTTCGTGCATGATAAGGGTGGAG 30230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGATGACGGTCAAGGATTCGGGCAGAAGCTTGTCGATGAGCACGGATGCACACTTGAC
                   CEF20D1 40600 bp DR Caenorhabditis elegans cosmid F20D1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29642. .29714
/gene-"W06D12.t1"
29642. .29714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted using tRNAscan-SE-1.11 preliminary prediction similar to tRNA-7?7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(29577. .29648)
/gene="W06D12.t2"
complement(29577. .29648)
/gene="W06D12.t2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVSDDIPPGFPRPQNNTKLQKSQKFSTDAMTSNSDYSADFLDDELEDEVDKMSRIPSV
TMNRLIRRDVAGGNTKLLADVDVAAPSVNVQDLPESEVGNPTGNRKFHVPTNASNDVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="Sptrembl:045890"
/translation="mQpaselpQsiQQLnddsapvckyevlmenaQgpplshatvgdl/translation="mQpaselpQsiQQLnddsapvckyevlmenaQgpplshatvgdlVYHKWSCDGNNKEMYCMTVHSCVVDDGQGFGQKLVDEHGCTLDAFILKELEYNEKELE AGQMSSVFKEADKPTVFFSCMLRVEMKESAEMPCVITTEVCKNLPSSKMQNLDVMTDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(28517...28645,28743...28885,28938...29044
29096....29211,30024...30152,30200...30467,30519...30661))
/gene="W06D12.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRNSGTQTTSOIKVASVQTAERYEQTWDEDPEEEQPKSRIMTRRLYIYNTGE"
complement(join(28517...28645,28743...28885,28938...29044
29096...29211,30024...30152,30200...30467,30519...30661))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNMLFYFVDHFWQNIGRQWIQSLRQKLRRRKVQSLEEGSIDKTPLMETSSTPPSPQNP
NGTRPIPLLLVLIVLFFWMIQCVAYFAYFENWTLFESVYFFFISMTTIGFGDFTPSHT
VAVGGIVFILGGLSVVSMCINVIQMQLEFIFNQIVQRIENDFKNTLSVAAEESRKKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTRTNLILSLLILAALGIVTISLMYLSLQVGKPKNYRSRTFRDEQFGYFFNFYFTGIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAB04922.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVSEFGSIDPSKKKTMRTDGNVAEKYSENMEMGNKLLMRFMSNHQKKMLNEKFDERAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="Sptrembl:045891"
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Slkhednmkvlktstlakovfyorlonmysgnossepsetklrrvlseydaamgisi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB04923.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA EST yk101g8.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="cDNA EST yk101g8.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="W06D12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e-"TTA ??? ?-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.8; DB 3;
Pred. No. 0.075;
0; Mismatches 112;
                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 34368;
                   complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                linear
                                                INV 13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29044,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence AL031620.

The true left end of clone C18B12 is at 40500 in this sequence. Start of this sequence (1. .104) overlaps with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F20D1.

It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The end of this sequence (40500. .40600) overlaps with the start of sequence {\tt AL031620}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neighbouring submissions.
The true left end of clone F20D1 is at 1 in this sequence. The true right end of clone F20D1 is at 4761 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap hetween neighbouring outside.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-AUG-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 ISA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; ADP-ribosylation factor; Cuticlin; Human mRNA KIAA0066 protein like; Transcriptional activator protein. Caenorhabditis elegans. Caenorhabditis elegans Caenorhabditis elegans Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278542
278542.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the specified clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       name-F20D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The C.elegans Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 40600)
                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                CDNA
                                                                                                                                                                                                                                                                                       CDNA
                                                                                                                                                                                                                                                                                                                                                                      complement(join(3587.
4490...4560))
                                                                                                                                                                                                                                                                                                                                                                                                                            4490. .4560)
/gene="F20D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(3587.
                                                                                                                                                                                                                                                                                                                   /note="predicted using
                                                                                                                                                                                                                                                                                                                                          /gene="F20D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="F20D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ∕organism="Caenorhabditis elegans'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:1507784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is NOT necessarily the entire insert of ed clone. It may be shorter because we only sequence
                                                                                     A EST EMBL: 2145;
A EST YK61b9.3
A EST YK61b9.5
A EST YK61b9.5
A EST YK327b8.3
A EST Yk327b8.3
A EST Yk327b8.3
A EST Yk327b8.5
A EST Yk3285.5
              EST
EST
ST yk6lab.5. comes from this gene ST yk6lab.5. comes from this gene ST yk327b8.3 comes from this gene ST yk327b8.5 comes from this gene ST yk327b8.5 comes from this gene ST yk314b2.5 comes from this gene ST yk318d5.5 comes from this gene ST yk315d5.5 comes from this gene ST yk413f2.5 comes from this gene ST yk416d2.5 comes from this gene ST yk416d2.5 comes from this gene
                                                                                                                                                                                                                                                                                    EMBL: Z14514
                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>.
                                                                                                                                                                                                                                                                comes
                                                                                                                                                                                                                                                                                       comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                .3770,4128. .4253,4308.
                                                                                                                                                                                                                                                                                                                      Genefinder
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sequence

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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB01744.2"
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IYGAMGLIPIFLCIELNTILGSGTIFASGVIYGFMALGKKADRSNMMAAGDPAWSPQV
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SDDEMAAGAAVDENPKEEILLSKEFTETFECQEVFRDGSINGHIALTRTHIYVLHDVP
GKQGYVTTEARHALSTVVAVTSRRSVPEMLTFKLGYEMNGSSKITAVHKLYVPKAGEC
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domain), Score=-49.5, E-value=0.00032, N=1
                                                                                                                                                                                                                                                                                                /gene="F20D1.3"
/note="cDNA EST EMBL:Z14943 comes
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12213. .126
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F20D1.3"
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NNA EST yk57d9.3 comes from this gene NNA EST yk57d9.5 comes from this gene NA EST yk174e5.5 comes from this gene NA EST yk145g5.5 comes from this gene NA EST yk145g5.3 comes from this gene NA EST yk484d5.3 comes from this gene NA EST yk484d5.5 comes from this gene NA EST yk484d5.5 comes from this gene NA EST yk484d5.5 comes from this gene
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.2608,12654. .12862)
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                                                                                                                                                                                                                                                                                                                                      ACGAAAATTGACAAATCTTACAAGGTTCAATGCTTTTACGCAGAGGCTCAAAAAACTGTG 31327
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EIVVMANWFGLQIWRINCMAESSQPPVAQFTVPGADLNHFYDGFLNGNIVFLSATPDG
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GFERLLDYWVLNTQTFQMLQIFSGMPCFLIEPRLTACHSGNIYVWGDFDQPLFCMPPN
GTHLRILRVSGLEKASHPPAYSTYNPAPPAYBSLDEKSGNPPYPSNPSNQPYPSNNYG
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/gene="F20D1.5"
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CDNA EST yk24a4.3 comes from this
CDNA EST yk39e3.3 comes from this
CDNA EST yk24a4.5 comes from this
CDNA EST yk39e3.5 comes from this
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/gene="F20D1.5"
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/gene="F20D1.10"
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A EST yk401a4.3 comes fr
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897 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9851916
2 (base
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On Jun 28, 2001 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-MAY-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-JUN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
5 (bases 1 to 26449)
                                                                                                                                                                                                                                           http://www.wormbase.org/db/seq/sequence?name=K06A1;class=Sequence
                                                                                                                                                                                                                                                                                                        For a graphical representation of this cosmid sequence
                                                                                                                                                                                                                                                                                                                                                                      more than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neighboring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUN-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
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Direct Submission
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Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U23449.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 26449)
                                                             5' cosmid is K03H9, 900 bp overlap; the 3' cosmid is T28D9, 0 bp overlap. Actual start of this cosmid is at base position of K06Al; actual end is at 16582 of T28D9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 26449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanger Centre, Hinxton Hall Cambridge CB10 IRO, England email: rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Department of Genetics, Washington University
St. Louis, MO 63110, USA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 to 26449)
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                                                                                                                                                                                         NEIGHBORING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cosmid K06A1, complete sequence.
                                                                                                                                                                                         COSMID INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cosmid K06A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replaced gi:733545
                                                                                                                                                                                                                                                                                                            and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  şt
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                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Hypothetical protein K06A1.3"
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NLIYNENRTKAFVNSNAFNFPDQNNVRISCKISVCPTLSGTCHQPKCDASASSIDDAS
EPIGKELARDELITTPMPTSSTEIPSTTTTSTTTSTTTATETPTTTEREPTTTVTQ
VLDPTTTVTLPTDFTPDSIFRLLKSPKKSNNTVWEDDAEGSGIEISEGSPAHAEAQHM
TSSEGPRTTKREIKRRDATDVDEHRQISYLPASVSLVADVILNFARCRFTNVSLKFIL
LKVCFYMYFSSRHAGRPTGSQMQPFHYLRGYLLNSKNPRSLSSGSSNQCINNQNGNNQ
TSSEGFTTKREIKRRDATDVDEHRQISYLPASVSLVADVILNFARCRFTNVSLKFIL
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5430. .5545,5594. .5725,5773. .5969,6018. .6415,6852.
7072. .7234,8113. .8457))
                                                                                                                                                                                                                                       PPGKEISIEVEQCTRAESPTLNHNILIEWFPLDSTPPTGDLQRLWSKPYLVPQSHWQY
FVLPYYVDDSVTSYSPSHVSSVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="for a graphical representation of this gene see: http://www.wormbase.org/db/seq/sequence?name=K06A1.2;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTSDICFSHFHATSEGDIERFDCSQKPSKLSTLSCAVLLIKTDESSYCLGDARDTHCC
CTSSSSPKICAPEKRKMAELTQLWTMSQVWWLVFGHVGLSCVVLLLVTFYMKSVKYLP
KYNIVIPEESRWTTILWAKIFDAGIGPSLYFSFPLIFFIFDFSLFIYVKDRKYINKFG
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http://www.wormbase.org/db/seg/seguence?name=K06Al.4;class
                                                                                                                                                                                                         complement(5030. .8457)
                                                                                                                                                                                                                                                                                                                                                          /product="Hypothetical protein K06A1.2"
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/db_xref="GI:733547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4644. .4803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALFLAIFKLITVPIFVYECFLSTVCLWHKDHEPGYCRLNGAIWQFMVFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to C. elegans cuticulin precursor; coded
for by the following C. elegans cDNAs: yk334a2.3, cm20c2,
yk60c1.5, yk334a2.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join(y8. .182,258. .358,462. .536,656. .798,896. .1277,
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IESEFNEWTYIHPRPFHVPRLGLSILNVKNNRNNDWLALRALLSTTGFYKLYPSKFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join (4.064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="K06A1.2"
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http://www.wormbase.org/db/seq/sequence?name=K06A1.3;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
/strain="Bristol N2"
/db_xref="taxon:6239"
                                                                                                                                                                             /gene="nhr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             =Sequence*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="K06A1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="K06Al"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 26449
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.6983

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Matches
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Best Local
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                                                                                           779
                                                                                                                                                                                                                                                 331 ACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTT 390
                                                                                                                                                                                                                                                                                                                                                                                                     271 AATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTTGTT 330
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 82; Conserv
                                                                                                                                                      AGTGCACAGATTGAGGT 407
                                                                                        GGTGCTGAGGTTTCTGT 795
                                                                                                                                                                                                                                                                                                                                          AATCCGAAAGGAATGGCATATACAGCTACAGTAGTAGTTCAGCTTCATCCACTCTTCACA 718
                                                                                                                                                                                                             ACTAAAGTCGACAGAGCCTATAAACTTCGTTGTTTCTACAAAGAAGCCGAAAAGGCAGTC 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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OEKSAEFMNELAELKEENSVINTERVSLVATCNXLTEKSAEGTSPETLDEFMMT
DVLPSEVKFKLSTHDGEVHDVEMMSDDTFATAGSDSKVQIWRVSPNKTDASKVSTLSG
CLGPVURRLDVDSORHVCLASSNDKTCRLMNIDSORLLSTESGHTDKVSSARLFQSHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=K06A1.1;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISGSADRTIKNWDISSIRCLKSYLVGSTVFDIVAKCGVSQSSFISSHFDKKVRFWDAR
SSDATYSVELGQKVSSLDISMDGLQVLASSRDDTLSLIDVRNYGIIHLYSAEQYKTSC
DSTAAIFSSTGEYVLAGSSNSSVFIWNTKTTKLEKVVKTARSDSAQIMSLAWNPSGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(9832. .9922,10394. .10716,10769. .10943, 10993. .11636,11686. .11847))
/gene="K06A1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="for a graphical representation of this gene see:
http://www.wormbase.org/db/seq/sequence?name=K06A1.5;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(9832. .11847)
/gene="K06A1.5"
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VYRMACAVDSMLASAYYSYKVGIEKERLILFNGDYINMNPIPISGDEPGAGTEFQTPQ
EHEKYKTLMPLKLKQYFDLAIPFARLEVSFEEYVLLKALIIWQISNYRLLEEGRAICA
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CLDAGMRRELVQARKEETRVAKRRSKGLYVSKKEDDDVBSSYBEYNTYTNVQDSSPK
MESGINEMT1 FESYLLSPDSSSOPLDMTVTPPPLHRSTPSILLTPATGBRHCQBVLS
NSPPFDIHQASTSHAGFIQHVQFYPVEVENKIFELVDHYVRTEASLNDRRKIMYTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence K06A1.4)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Contains similarity to Pfam domain: PF00400
(G-beta), Score=70.8, E-value=9.6e-18, N=5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -Sequence*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSTDLLYEYFYPPTDLFKNTFEDVPPSPESLDVGDSLGSSPSYD
LGFQPSFDIDFCIWKEGSSSPPPESNHLPEIVNKASTSPRGMPSPLTDSRSCHVCSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to C4-type zinc finger domain (exon 2);
coded for by the following C. elegans cDNAs: yk325g8.5,
yk324h4.5, yk324h4.3, yk325g8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to transcription factor AP-2 (SP:TAP2_HUMAN, P05549)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(13643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="K06A1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="K06A1.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .14066,14112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 3;
Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .14328,14377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 26449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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CDS

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TITLE
JOURNAL
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AUTHORS
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AUTHORS
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DEFINITION
ACCESSION
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TITLE
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MEDLINE
PUBMED
                                                                                                                                                                       TITLE
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                                                                                                                                                       JOURNAL
                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                           The sequence of C. elegans cosmid K03H9 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis 1 (bases 1 to 31731)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                                                     Submitted by:
                                                                                                                                       University,
                                                                                                                                                   Submitted (23-MAY-2002) Department of Genetics, Washington
                                                                                                                                                                       Direct
                                                                                                                                                                                         Waterston, R.
                                                                                                                                                                                                                         Submitted (13-JUL-1995)
                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                Anderson, K.
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                                                                                                                     Louis, MO
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                Department of Genetics, Was
St. Louis , MO 63110, USA,
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
                                                                                                                                                                       Submission
                                                                                   Genome Sequencing Center
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                  63110, USA
                                                                                                                                   Genome Sequencing Center, 4444 Forest Park Avenue, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31731 bp DNA LINCOL COSMID KO3H9, complete sequence.
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                                            USA,
                                                                 Washington University
                                                 and
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NOTICE: This sequence may not be the entire insert of this clor It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions. This sequence may not be the entire insert of this clone

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

http://www.wormbase.org/db/seq/sequence?name=K03H9;class=Sequence analysis see: For a graphical representation of this cosmid sequence and its

## NEIGHBORING COSMID INFORMATION

The 5' cosmid is T25D10, 200 bp overlap; the 3' cosmid is K06A1, 900 bp overlap. Actual start of this cosmid is at base position of K03H9; actual end is at 8345 of K06A1.

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE\_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from Blastx analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers.tRNAs

RESULT U21318

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                                                                                                                        FSFSYHDYNELNREKIPISVDGRSGLLETFKDKSKLPVEKVPEDVLWEKALDSMSYEE
ARSSIVQALRENSNSSLLHIRACKLEKSSESQYEWIKLALLNDKLDNRMQMLMYAKKK
CRPHTYRKVLKEGNY<sup>8</sup>
1 5461 c 5708 g 10092 t
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http://www.wormbase.org/db/seq/sequence?name=K03H9.1;class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MRASPLLSLSIFITFVSIFSLLTYLPSFFAQISRIERQLEEELD
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MNGERGSTGLDGAPGEPGSPGLPGFAGLPGSIGITGIKGVMGEVGEPGAPGIPGEEGL
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ESFylakekraaaialkrecsfolsyasykropheaiasiyolikeepyefder
NSINNTSLKELMAKKHEDKRESTGETMIKNIKLLYENBOLDESLHLDSRSOQYVMYEN
VSPETANATEISIAKNLSICSTECIAKDTTTPKEFPSCLFPTFLEKNOAPVEKRSVEY
VWKLALDGMCYVDARVAVVQALREYPNSSILEKKAVOLENTLDEKAKHIEFALROKEL
DDRMVIVKRADGLEFREKYLECILNAVTOFFANLDIVHELCILLAESTGEFLDYVDLK
TALDNNKMSEDOFIOLYLKSEKCGSSLYRKKYVDKYISYTPFTTENFGNWISLITTLH
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/note="for a graphical representation of this gene
/note="for a graphical representation of this gene
http://www.wormbase.org/db/seq/sequence?name=K03H9.
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1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
gamma 2 (SP:PIP5_HUMAN, P16885)"
                                                                                                                                                                                                                         translation="MTKFKKETKLDLEVFYDKYTLHYIIALADIQKRLRDTIQLAVEN/
                                                                                                                                                                                                                                                                                                                                /codon_start=1
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13778.
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http://www.wormbase.org/db/seq/sequence?name=K03H9.3;class
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/gene="K03H9.3"
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/strain="Bristol N2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-OCT-2000) Blanchard A., INRA, Centre de Recherche de Bordeaux, Institut de Biologie Vegetale Moleculaire, 71 avenue Edouard Bourleaux, BP 81, 33883, Villenave D'Ornon, Cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327650 bp
Mycoplasma pulmonis (strain UAB
AL445563 AL445566
AL445563.1 GI:14089413
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                                                                                                                                                                                                                                                /translation="MSKKSLDKIDLLAYNKTLQDIFESKINDSMLYQNIFKFLEITKV
TFDQVK.AAPNQDVINHLNSDFKEDIKOCIFQLFGENREITFTSGKKDSSESPKKSEE
NIQLYBESQNNDELIKKFTFDNFIQSKFNENAFLIGKEIILBNFGIYNFVLISGDSGLF
KTHLLMAIGNEFLKKYFKSIVKFLTFSDFYRKIMFILSSNNINENAKKFKELTEADLV
MFDDFQIFSIGNKRATLNFIFEILDKRIMNNKYTILTSDKDLKFMASLFEQRLYTRLS
                                                                                                /gene="MYPU_0020"
1741. .2862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="dnaA"
/note="identified by sequence similarity;
similar to SWISS-PROT:P34028 (DNAA_SPICI)
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/standard_name="dnan"
/note="identified by sequence similarity; putative;
                                                     /gene="MYPU_0020"
/EC_number="2.7.7.7"
                                                                                                                                                               TTLRSKINKLS"
                                                                                                                                                                                     SNLVVARDMAIYLIREDLNYSFSRIGLIFSNRDHSTIFNSHRKISQSINSHDSTKYTI
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                                                                                                                                                                                                                              SGLSVETEQPNKEDMLKILKFQLKIKNLSPEKWEKDALDFMVRNFSKSIRFLEGALDK
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/db_xref="GI:14089414"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MYPU_0010"
222. .1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mycoplasma pulmonis"
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/db_xref="taxon:2107"
                                                                                                                                                                                                                                                                                                                                                                                  /product="CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA"
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/transl_table=4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ′codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA linear BCT 14-MAY-2001 CTIP) complete genome; segment 1/3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               possible;
Blastp2 P=6e-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="MYPU_0050"
complement(3778. .4422)
/gene="MYPU_050"
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/db_xref="GI:14089418"
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LKKIKSFKSLKNLFIYQINKKNKEIKNSSLFKKIFNLFPININKAIYSIYSSKHOGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="g1:14089417"
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Kindivnhedeykylknedylfynnevyvikkwfdgbhfkankeslkkllydilekfws
Qnldlakmnwlfyktkdpkylslvekykddfndvihgdlnfknilandknevklidfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="identified by sequence similarity;
similar to SWISS-PROT:P43055 (YLI1_MYCHO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identified by sequence similarity;
similar to SWISS-PROT:P05650 (YAAA_BACSU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNLSLKNNILTLVATNRARIAMOKIKTEDSQEFNLTINSKVYKELISLSMSNTLILSP
GTFELKIKSGNLEIKTKVIEIPYMNVENVFPNKFNFVIHIDKKELLSLIDKVSIVNDE
KNGNKILIEVNPSKKEKKLKLSSYWPDLGFSEVFSDNFEVESEILLKFFINANYLKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="DNA POLYMERASE III, BETA CHAIN"
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/db_xref="G1:14089415"
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SDLQSYEINLLDHEREPDIKFGLNNSQLQLKTEQFKQALKNVVFAADLSNAQELLLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTILIKGEFLTIGQLIKKIKLIDSGGQIKQFMQSHQVKINGKLI
NTRNTKVRVGDTIWIDDQLYTIKAQNNEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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/note="no -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="CAC13177.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIKKGSKYFDIICIYKNFNINKNELIKRFDLNEEKFDDYLYMSVKFIEEAEEKVYSKM
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                                                                                evidence=not_experimental
                                                                                                        codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="no similarity found"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MYPU_0040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MYPU_0040"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MYPU_0030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           possible;
Blastp2 P=1e-28
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Blastp2 P=6e-06
Query Match
Best Local S
Matches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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al Similarity
154; Conserv
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MYPU_0080"
/standard_name="hit"
/note="identified by sequence similarity;
similar to SWISS-PROT:p32083 (YHIT_MYCHR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8190.
                                                                                                                                                                                                                                                                                                                  /standard_name="rplK"
/note="identified by sequence similarity;
similar to SWISS-PROT:P75550 (RL11_MYCPN)
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IPKKHSTNLKDIEEQSINHLMKIAIKLAKEKIENKEFEDFKLIINNGEKAGQVVYHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                 8643. .9296
                                                                                                                               /protein_id="CAC13182.1"
/db_xref="GI:14089422"
                                                                                                                                                                                      /product="50S RIBOSOMAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                               /gene="MYPU_0090"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MYPU_0090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHIIPFRKKEGHEH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="HIT-LIKE PROTEIN (CELL CYCLE REGULATION)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/transl_table=4
                                                                                                                                                                                                            transl_table=4
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                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                        translation="MEVDQWLTQLPHILERIVLIMAKKEVVKIAKLQFIAGQAKPGPS/
                      4.2%;
46.7%;
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possible; Blastp2 P=7e-22

0

Score 48.4; DB 1; Pred. No. 0.77; 0; Mismatches 176;

176;

0;

Gaps

0

Length 327650; Indels

possible; Blastp2 P=6e-36

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RLNDEYRKANETQNSRLNPELIRAFTNVETTTENAGDLNYNIDQLKEQKEVINGFLYD
KNKIISNKQLLINQASQSGTGDLTRFIQITNFKDGKSEIDMSYILKLTPLFEEDTAKT
AEYNNDKKDSDPTIKRGFFTFKNTPWDPDKAESANELTKLAYWLYRTDNSLFTQAKNH
                                                                                                                                                                                                                                                                                                                                     KKTSTKESYLNLYYEYIVSQKYSNDSIDFSTKNDQSLDDKNSQFYKDAFLAYKFYVSN
ERLKKSTWFVDQRANWEKANITSFVNKTTNQSITMNFGHPLDENNFKVLFLNKTSPVR
HEIIKMLMVKNYLLNTSEEQVKKSFPDYENKIKLLDKNNTDKKIYESIDLSKNNFFLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="identified by sequence similarity; putative; similar to TREMBL:049557 (049557) Blastp2 P=3e-15 C=298 pfscan: pos. 18-28 PS00013 | PROKAR LIPOPROTEIN Prokaryotic membrane lipoprotein lipid attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISYSAFNPDRQLGDATNNNTGVDLILNKAKNYKGVETLFSNISAETRRQADIDQHIIN
VASVNUSKINGRGFVGFGSLLDVSTKTSDLLSLTILGGIFKVAELDTAIN KNPLDTFIE
KYKENEPGLLDAAPHVSDVAATNNETSQKIQDMSKEEFDIKIKKIFATTTPFDFG
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8190. .8540
                                                                                                                                                                                                                                                                                             KYLLKDKRMIMKWNYKSETDSSKVLAGIDVYINNIQEFNENVQTQSRVESLLTEDISL
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/protein_id="CAC13180.1"
/db_xref="GE1:14089420"
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6759. .8189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSEPEKTVDSMKSFFENILYPMFFDVFGSRRLKGDN" 6759. .8189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSSSTQRVGFDTPKLLKYFSNDTFAAQGTFSNAEFEKFYREKYSNLTVENFNSEKEN
ARAHFLRNITNHDFSNQSKEVEKIRKFIESEKDKNTYVELNDENIFKLKYPNNDINTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVNNSTAQRRALPGDAPLFNET INGRNSDQVTSTVDSVLNQGVLKEVKKQEEVFTKWSN
AYSEFLYEQERKASULANVFKVESGFSKYESETHVKK I DELIRASERKELDDAKRN
IQLQGGPANWEAEWILKQLRENDKYGKKGNEEDALEFLYQKK I KNDAYRREDPQILSSL
NVDDLKKVASRDIMDIHDNTKVFIKKGQPLFPFAFDGTNLKQNVVFHSNDSTNKSARV
                                                                                                                          FSSIGYKIESNNPIIRDLLKNEGILK"
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CDS

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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAGGTATTGATATATATATTGAGATTTTCTATTAATTCATACAATTGGTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTC 227
                                                                                                                                                                                                                                                                  Direct Submission
Submitted (18 MAY-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
(http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
                                                                                                                    Agency: Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 53150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota, Mycetozoa, Dictyosteliida; Dictyostelium.
1 (bases 1 to 53150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC116984 53150 bp DNA linear HTG 18-MAY-2 Dictyostelium discoideum chromosome 2 map 3000630-3053778 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                         Funding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noegel, A.A.
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                                                                                                                                                                                                                                                           http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 53150)
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/db_xref="taxon:44689"
/chromosome="2"
                                           /strain="AX4"
                                                         /organism="Dictyostelium
                                                                                                      Location/Qualifiers
                                                                discoideum"
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CDS

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GFDKILFSLESNTTLTNLNLSKNQLDLSIPLNYLTSSLAFNKTLTSLNLSECNLQNSH
FIQISIALQSNKKLKKLNLSKHKFKSNDLFILLNYIFKLNDTVTLENGNIIDIDIPSI
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SVNGLEYLGRALSNNQTLEKLIWSYNQSNYTSVMCLSNGLRNPHSQMKSLIMKGCDIE
GWGALSLADTLAINKSLKELDLGSNQFGDAGAITLASKLNSHPSLSILDLSSNLISTE
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LPNQLEPIVRÞSQQSLEAQREKNSNNFFIYSPYGGFSNGSSIGGGGIGGGSGGDSN
SNRKKVVMQGGEECSVVTLSNPFSPOD FIQSLTLSTAVPFESSPLSFRKILSLTDSN
DIVISKRLESGPLIIKGVFVRAVNLLSEHPVDPYGNSISISQYNELVRIGDAYKVDI
LEFDSTTTASNNTSSFSRDNNNNNELPIVNKIKATPKLPIKLPIKAVPTLGKVLNLLAGE
SFSTRLEFQNIGTTQIDSISVSLNEFDKALKKTLADNUQYTTDSDDETISGQMDSNI
IKSSLPLLEGETFKLPIKSFSKFLIGNQFIIDYSNCENEEEBEEFNNTTTTTNVNT
GTLTVMGNTQSTETATTTTANKYQRKITIPLPLSTTHEGPQVLNEDIVYASSKIIKSL
                                                                                                                                                                                                  KASCRSLILSLNNLEANTFRITHYTYLKKLEIINNINNDSDYSDFDDSDDDDSDGDDN
RKDYSNDDIYYDYFDQKKNMTYRRRKRVLNDNSDKIGKCLATIINLSLPNLSTLNLSM
                                                                                                                                                                                                                                                                                  /translation="MDVQMYIKDEDQEIICLNNDISLIEIDNDDDQDDEIFISPFVKG
QSIIHKILPIHIMQIIFYYTLTLGEFNSNEETVLKIWDSKNNDRYSLEAVCVTWCSII
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/db_xref="GI:20976604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLIQFKNNKQLVKTIEQGGFETIEVLVTNLTNTPINGLVLHILPIIDQTNNNNNNNNN
NNGNIVDVSNKLGYIGSLTTPIQELPVGATFNHSLDVIFFERESYKFIISCEIFKTKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGIPNIVDNNKEINNNLSSKFILSPNGIITIIVPMKRESLPDQLPPLRQAKGQYIKPK
KKLTEYEEYVKCLIQYYKDLLTSKIKLLWNSSDNTNGSILLDNIVLTSKLIHKLNKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNKRKYPOPEVDVMLKFANYHISMORRIEASELLTMAYDFGKULSFTPRITLGCSIA
LLYYSMGFRRKFAFYLREAAFLYNTRÞENWEKINHLLIASKYYGLEDLFSNSPSRFL
DEGGSKKSHLSFTLKOMKKSNSVTSGRNNNNNGGGGGGGGGSNGNNSKNSSSPTNVFG
AQYNQFNQSIQQQVQSNSSNRSSSSSSSTSNFTNNIÞELSYRKÞKFGWSVIQRYLIYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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KDLQETKRLFEIAVAQYPSCVSSLCCAFDPMDDQPDLGLGANLIMIPNNSDRKHLIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(144. .2404,2450. .4378,4501. .4660))
/note="ORF_ID:dd_02769"
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/db_xref="GI:20976603"
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complement(join(10585. .10678,10842.
/note="ORF\_ID:dd\_02772" YDNYDNYDDGGSGGLGGSELQARALYDYESAEPSDLNLKAGDIISVIQQDDGSGWTKG RNYEGNEGIFPSTYIEYV" QLPLEMESMISKQERTLVQIQPQGDTGSDAYRISYAPGTIQTTGGGDQYYESYESYDN DDQKATATFEKNYKKDRDQMRQDILKLEAKTRKAGKKTTPEVLKQQITELNDKIKESE QLNANKLRDVVLMERRKHATFLSQFNQFLEKETELSADTMSKFSTNLNTHRDLINSQS IHQLEYIDLSLPHEPLTKNINLLLREFRKNLKVNSPPLFTEVIKAANKYQQQAQALSQ AGLVLADTLTRLTIHNGGDFGEGFKKLADAIKDLENRDDVAKVLLNEFITPNKQAIE /codon\_start=1 .10913,11037. .11212))

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CDS

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11 protein"

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CDS

Pichia pastoris" /product="putative protein ubiquitin-conjugating enzyme,

/protein\_id="AAM33195.1" /db\_xref="GI:20976606"

translation≃"MAARLMKEYKVLQNEEFEDILLYPRDESDLYRWVAIIKGPPDTP

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CDS
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SSSREMINVSLEVLRKDLEFVLSILSDQIKSPTYSEEELRQIIVCIIRVEMITNSSS
DQLMTEILMGVAFGDAGLGNLVIATPEDQQQNITREKLEDALRKYYVGKNIVIIVTSYGSA
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/protein_id="AAM33200.1"
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                                                                                                                                                                                                                                                                                                                                                                           FNIILTILFILFWLITKIISEHSFGGFISLIWYYSFMYGGGFGVVPAFLIDLFGTKNI
STCHALILTSWNLSGVCGGFIFTGIYDTLRNQYHYKVDNPILYNINFYWVSCVIMVGW
VCSFFIPVKIKYRLYPPIPNQLLQFTIFNRIFRIIKNKKNPFQLVSKEKENEEWNNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISPKIVSEYVYQSENSKLPSE" complement(join(18484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mesyknriyktqehvhhqdhsyqdcnhpkslkseskiirsdyqt
LADHSESWMDSYQDMQTKWEYLANTINSFGGGLYIDNSRIHELSEGFHRLQNLMFPIL
KTTKIGIHDNAEIISHHSVEKLKKQNHQMENNRVRADHATHKLDKYRSKSKTNPTTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKNKSOPPPKKNRIVWDEENLTINDMNKSSTMKIDEPKTPYHYYESEEETDESKKYLE
NKFLELQNALDROOEKSEWDSONDEOQOEKEKEKKKKKKKLKINKRSDSDDNDDNE
DEDEDETEKKENKKKPOLRKARDVEFKVVPDEON
COMPLEMENT ()OIN (16148. .16663,16774. .17016,17117. .17599))
//note="ORE_ID:dd_02781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="AAM33197.1"
/db_xref="GI:20976608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(14699..15027,15131..15587))
/note="ORF_ID:dd_02779"
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AIPILMNNDNNNNKTEQTTTTTIIKNTIFNNKTISFGRIGFRSIVIFLILVPY
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YLLHDISSTDSNDHKKMCNKCNHQKEPRAHHCRYCNRCVLRMDHHCQWLQNLGLISPOY
KYFYLFLFYTSISIIYFFTLLIKRSIELVTKYTMEKTLPSFDLLHLFLLGILIIILII
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Join(13214 ...13969,14095. ..14424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKSTYVSSNTTNAGDLSTSTSTSTTFYENPQTQPAEKNIIIPTIIKETSAPSSSTSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRLSLDQKPVKEKLHSRFGLIDQSLPPTYEKYHSNWIPKDHNYPVPHGSIIFDEKDDA
SSNDDKESEQTIEETTTTTTTTYEVPKGTKIDDLKMDEGTSSSFKRLSVSETNSPIQ
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EIVKSTTVSPFTPLNILHPKLVGEKLYSNDNEANNNQKEFKAEISTLPNGIRVVSKQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKEAVAEKATIIYDDSYRKYQHDIRDLEFKSVDNLHFSRQLLFDLQSFFNHGYEVVHS
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                                                                                                                                                                                                                                                                                                           /note="ORF_ID:dd_02768"
                                                                                                                                                                                                                                                                                                                                                    INYNKSLNLENNNDNNNNNNNNNNNNNNNNNNTNTPTSSSSNSNNKII"
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                                                                                                                                                                                                                                                                                       /codon_start=1
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTGCAACATAATGGACAACCTGTAATACTTGCTGCA 1041
                                                                                                                                                                                                                               Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadore
Rhabditoidea; Rhabditidae; Peloderinae;
2 (bases 1 to 45713)
Tin-Wollam,A., Sutterer,C.
The sequence of C. elegans
Unpublished (2001)
                                                                                                                              Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans AF067608
                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                 AF067608
                                                                                       9851916
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NCHAPLFVFNKVSLFGISLTTQSGFLQDGIELVLQELLMLRSSMTQQELERAKRSQKS
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                                                                                                                                                                          . 25635)
2;
Length 53150;
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Score 48.2; DB Pred. No. 0.89; Mismatches 0; Gaps

0,

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AGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAG 764 AGAATTTATAAAACATCAAGTCAATAATGATGAGGAAGAAGAAGATATTACATTATTTAA 29555

TATTACCATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGG TAAAAATAAAAATAAAAATAAAAAAGTTTCAAAAGAACACAAGAGGATAAAACATAAAAG 824 29675

ATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCG 884

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TAATATTAATGAGATTGGTTATAAAGAACCATCACCAATTCAAATGCAAGTTATACCAAT 29855 CACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACT 1004

29892

45713 bp DNA LIN cosmid B0511, complete sequence INV 19-APR-2002

Chromadorea; Rhabditida; Caenorhabditis

and Ozersky,P cosmid B0511

Sequencing Consortium

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REFERENCE
AUTHORS
TITLE
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   similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggs using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and
                                                                                                                                                                                     Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (22-MAY-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 45713)
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Submitted (30-AUG-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 1 to 45713) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (www.wormbase.org/db/seq/sequence?name=B0511;class=Sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For a graphical representation of this cosmid sequence and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neighboring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-APR-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, Mo 63110, USA Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5' cosmid is C43H8, 2850 bp overlap; the 3' cosmid is C34B2, bp overlap. Actual start of this cosmid is at base position 7 of B0511; actual end is at 45613 of B0511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Genetics, Washington University St. Louis , MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CBIO IRQ, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIGHBORING COSMID INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rw@nematode.wustl.edu and jes@sanger.ac.uk
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Location/Qualifiers
                                                                                                                                                                                  FHA.hmm, score: 28.36); coded for by the following C. elegans cDNAs: yk393e11.3, yk465a3.3, yk465a3.5, yk728a2.
                                                                                                                                                                                                                                                                                                        complement(join(6442. .6918,7008. .7178,7262.
7486. .7585,7641. .7694,7739. .7843))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(6442. .7843)
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2842. .29
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                                                         /product="Hypothetical
/protein_id="AAC17655.1
/db_xref="GI:3165537"
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DEPREY IHRVGRTARGTNGSGKALLVLRPEELGFLRY LKAAKVTLNEFEEFSWSKVANI
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vhekaeeatyeglqqgyivapsdkrllllftplkknktkkwyffsScnsykfhhell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to DEAD-box helicases (Pfam: DEAD.hmm, /note="similar to DEAD-box helicases"); code score: 262.89) (Pfam: helicase_C.hmm, score: 76.21); code for by the following C. elegans cDNAs: cm01c4, yk92g5.3, yk92g5.5, CEEST07F, CEEST27F, CEEST27R, yk290h4.5, yk39le3.3, yk39le3.5, yk461a5.5, yk462d1.3, yk482d1.5, yk483a8.5, yk727e5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="for a graphical representation of this gene see:
{www.wormbase.org/db/seq/sequence?name=B0511.7;class=Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Hypothetical protein B0511.5"
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                                                                                                                                                                                                                                                                           /note="similar to forkhead-associated (FHA) domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {	t RSKIIDSEGCSLDTTRLPNLRYENNKLSARVMSKAFRFGDDVAVEFECNVRLDLRNGT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="for a graphical representation of this gene see: www.wormbase.org/db/seq/sequence?name=B0511.5;class=Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein B0511.6"
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/db_xref="G1:15375231"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="B0511.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVDLPISNKPKVEIRSKLSGAGYRKKKQSFTFKAKK"
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/gene="B0511.6"
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{www.wormbase.org/db/seq/sequence?name=B0511.6;class=Seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4812,4910.
                                                                                            1 protein B0511.7"
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ACCESSION
VERSION
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CET22C8/c
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Best Local
           JOURNAL
                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGAAAAAGGTGCAGGATATACGTCATCTGTCAATATTGTCATTTCATTCCACGATAAATT 5087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGACCAAAGTTGATCGGGTATGTTG 5114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGACGTGTATTCGTATTGGGTCATTCTCAAGACAAAGATTGTGTATCTCGTGAAACTGG 4967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
                                                                                                                                     HTG; C2H2 type zinc finger; Cuticulin; Hyaluronidase; Leu-trNA, Mu-type opioid receptor; Transfer-RNA. Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
     Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortiun Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                   Z49071.1
                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
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                                                                                            none
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPSEILQIMVYIFGGIGILAKMYNDLITPAPLEWNVNNIAVCTAIILVMIINVVALIF
TIFWCLRSKDEGGEIDSNGVVINQFVEPNIRMKFKMPKIRGDAIHDSSQDVFELRVPR
NGNQFDACHEQTVIVARNKRSRTYSVPLESRPRTQSTGSEQIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAGRPVFEAYAERFKKLFGDNEKVITLAGNHDLGFHYALVQTFATHLTPTVELKNYLL
IMPETLEMFKKEFRRGLIDEMKIKKHRFVLINSMAMHGDGCRLCHEAELILEKIKSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="miwlknlrvpillaiilvvyneyfiffiafsscQwpckygrcse
SSVKAFMISDTHLLGKINGHwLDKLKREwQMYQSFWISTWIHSPDVTFfLGDLMDEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(8215. .8321,8456. .8774,9421. 9547. .9829,9887. .10105,10175. .10531,10581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTFISLSFFRHGTLGKIQDFWLKLANEKFFEQLLRSFIIKLHQTSYNTAQNRRIPQLP
ISVEEARRKKRPRGNVAFLEEEEVINEDVDDSVGRENLVTTAIISTWNKRPGDPK
RSEPPRKIVRPGRELMSAPLSSTFGPMALNAAPDLELYGKLLPEPGHHQYVTSTATED
EADDHHKKRYAKEAWPGRKPGAGIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(11495. .13652)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKNRPIVLQHFPLYRKSDAECDQVDEQHEIDLKEMYREQWDTLSKESSLQIIDSLNPK
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/protein_id="AAK95863...
/db_xref="GI:15375229"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="for a graphical representation of this gene see:
{www.wormbase.org/db/seq/sequence?name=B0511.8;class=Seque
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|www.wormbase.org/db/seq/sequence?name=B0511.13;class=Sequ
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51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                        27770 bp DNA linear INV cosmid T22C8, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
        elegans Sequencing Consortium (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein B0511.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 45713;
1.7;
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.10702))
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REMARK
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone T22C8. It may be shorter because we only sequence overlapping sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99069613
9851916
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-APR-1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 21, 1995 this sequence version replaced gi:780210.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neighbouring submissions.

The true left end of clone T22C8 is at 1 in this sequence. The true right end of clone T22C8 is at 8577 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The C.elegans Sequencing Consortium.
2. (bases 1 to 27770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence Z54284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The end of this sequence (27655. .27770) overlaps with the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          start of this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence Z54284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       true right end of clone T18F6 is at 5289 in this sequence. The rt of this sequence (1. .97) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or longer because we arrange for a small overlap between
                                                                                                                 complement(join(1838.
2686. .2785,3272. .352
4366. .4433))
                                                                                                                                                                                                                                                ANTKKLCCGCCAWLFKDEQKERTVVTF"
complement(join(1838..2075,
2686..2785,3272..3522,3648
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:Q22674"
/translation="MLLDSDEESTNRYWYKVGSYGIMLTEQASLYFTLLMTINREAVE
/translation="MLLDSDEESTNRYWYKVGSYGIMLTEQASLYFTLLMTINREAVE
VFPSILSVFTTKGIHIISTFIWYYINFIVFWYKNFGTTKTFSRKTISMKEVLLGTNIL
                                                                                                                                                                                                                                                                                                                                                                                              TKFFTLSSTCLPIAMLGMYLVIFIFIVKKRQIADNTNQKKTDRDTSLVVQALIITIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA88873.1"
/db_xref="GI:3879997"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/note="contains similarity to Pfam domain: PF01630 (Hyaluronidase), Score=706.2, E-value=4.8e-209, N=1cDNA EST EMBL:T00170 comes from this gene
                                                                                                                                                                                                                                                                                                                                          TIFCYCTTISNQLVNPLFFLTVNKMVRSVAKHIFDKNISSFLSDTSSTNKVPDRRRIQ
                                                                                                                                                                                                                                                                                                                                                                    EVILNNSVIISLVRHFLTLLKIAWLFVQNRLLELHCVNITDILTPLFKNADLSIQWIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="weak similarity with mu-type opioid receptor (Swiss
Prot accession number (P33535)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T22C8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1534. .1634)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="T22C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .489,539. .838,892. .1164,1211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489,539. .838,892. .1164,1211. .1296,1347.
                                                                                                                                                                                                                                                      838. .2075,2231. .2451,2502. .3522,3648. .3788,3925. .40
                                                                                                                                              338. .2075,2231. .2451,2502. .2618, .3522,3648. .3788,3925. .4040,4092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1296,1347.
                                                                                                                                                                                                                                                            .4040,4092.
                                                                                                                                                                                                                                                                                   .2618
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.4216

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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:Q22677"
/translation="MTVFSELEPSTFCSLVVVIVICSTSLLTHCTTAFFKESLKYVFI
/translation="MTVFSELEPSTFCSLOVVIVICSTSLLTHCTTAFFKESLKYVFI
LRHLHQTPVFLSDMNTSMNSTSTSFGSDOMDIENHSPKLSGVAPKRRRIDKSSTSSEAK
IQRMEDAMKKKLEKEOKEKARLKKEEFTLKKKSTTAAAKKNKIVGAPSEDPKIRALQC
DICFALFKNADKKRHDHSHKDEPEVYCPMCNAPIKYKYNLKOHMNKCQPSGKEMEQG
DICFALFKNADKKRHDHSHKDEPEVYCPMCNAPIKYKYNLKOHMNKCQPSGKEMEQG
                                                                                                    complement(join(15072. .15356,15407. .1547(
15840. .16043,16127. .16221,16685. .16796)
                                                                                                                                                /gene="T22C8.6"
                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:Q22678"
/translation="MDGAATKFFRPWESHGSYHHSLPSISPPDSPASTSASSSSSSIG
ANELTTKRRKCERCTCPNCKAIKHGDRGSQHTHLCSVPGCGKTYKKTSHLRAHLRKHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="sptrembl:Q22676"
/translation="matteqlanttokepvidldodsnmeiahkiqnqtkrlpisepa
nknknvtskqnketnrktekssrmatstiqdrvlrigotrkokesttekvnatikks
akqikvreeeegdddlebeljvlysskrmmyssknrktikprndtiabegetdgehg
vkqrafdpkqrhrqcpeclillstpdkikrhmkshgdvpdvycsicntpikfkknyhlekcydkmkislhdsmlskyypdfvrklqeaaknpvlpmptlegmpveftlkgvvgf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="Sptrembl:Q22675"
/translation="mutwyholllulifigaakgaqyigsgasqpnrtdvvwnyps
wtckneysidvekygiiqoedqhfygggasqprrtdvvwnyps
wtckneysidvekygiiqoedqhfygggasqfripyekaqnesdpkngglip
QMGDLEAHLIQAEKDINETIDDENFNGIAVIDIEEFRPMWELSWGPFSYYKTESIRLT
RQOHPYWSTKQIEWQAERDYEKACQKFFIETLRIGKRLRPNAKWGYYLFPKCNGDVGQ
RSDTDCSTLFQKENDNLHWLWGESTALFPSITLYEKGKQNPEYNFUNGSALITETKRI
KRNYCPSCEILYFTKLEVPYYTPDDDFYSKQNLASTLDIAIKMNANSVYIWSTSQSIG
SRCGSIQTYVDNTLGPYIQLTDRNLDKCRMERCEGRGECYLPRPKTNPAIYNFACRCE
RPYFGKSCEYRGRRMGVSMPKASQTPQVIPDVTAYFSTSSNGTKKYNAPNQFYSRTGG
                                                                                                                                                                                                                                                      GDRPFVCDWFDCGKRFDRSDQLIRHKRTHTKEYRFACKFCIRQFSRSDHLQQHLTSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="722C8.5" foin()2022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMLAKAYPDYLRQLQEAAVNPSLPMPTLNGMPYRMDRYSFVTGFDMSLDVHLDVMLPK
YPTDVFVCNLQLYSEDEDALDDVNLFDEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(9764. .9814,9844. .10053,10113. 10428. .10872))
/gene-"T22C8.4"
                                                   /codon_start=
                                                                                  /gene="T22C8
                                                                                                                                                                                                                                       NIVVVD
                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA88877.1"
/db_xref="GI:3880001"
                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains similarity to Pfam domain: Pr00096 (Zinc finger, C2H2 type), Score=72.5, E-value=2.8e-18, N=3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )oin(12937. .13133,14103. .14201,14286. .14396,14608. .14701)
∕gene≂"T22C8.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA88876.1"
/db_xref="GI:3880000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains similarity to Pfam domain: PF00096 (Zinc finger, C2H2 type), Score=19.5, E-value=0.025, N=2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10428. .10872))
/gene="T22C8.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(9764. .9814,9844. .10053,10113. .10324,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTSLDITKDLMLAKYEOKKORELAGIDSDDSDELDYFDDFPDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains similarity to Pfam domain: pr00096 (Zinc finger, C2H2 type), Score=29.5, E-value=2.5e-05, N=2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(7754. .7819,7868. .8059,8139. .8350,
8608. .8952,9038. .9182))
/gene="T22C8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(7754...7819,7868...8059,8139...8350, 8608...8952,9038...9182))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIKLARKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA88875.1"
/db_xref="GI:387999"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="T22C8.3"
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/db_xref="GI:3879998"
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       _xref="GI:3880002"
                                                                                                                                                                                                        lement(join(15072.
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                                                                                                                                                                                                        .15356,15407.
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                                                                                                                                                                              .16796))
                                                                                                                              .15470,15586. .15728,
                                                                                                                                                                                                   .15470,15586.
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ORGANISM
                       REFERENCE
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AF455359
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                                                                                                                        AUTHORS
TITLE
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AUTHORS
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Best Local
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                                           unpublished
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                                                                                                                                                                                                                                                                                                                            AF455359.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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CDS

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451 CCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCT 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAAATGTCGATATGATGTACTCTCCGGTTCACTAAATGGTCCAGTTGTTCGATTTGCT 20154
                                                                                                                 Maccheroni, W. Jr., Joel, R., Bove, J.M. and Garnier, M. Identification, organization and expression of five mreB-like in Spiroplasma citri: Effect of mreBl disruption in insect
                                                                                                                                                                                  1 (bases 1 to 6942)
Maccheroni, W. Jr., J
                                                                                                                                                                                                                                                                                                       Spiroplasma citri
Spiroplasma citri
                                                                                                                                                                                                                                                                                                                                                                                                                           complete sequence.
AF455359
   Maccheroni, W. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF455359 6942 bp DNA linear BCT 11-
Spiroplasma citri GII3 cell shape-determining gene cluster,
                                                                                         transmission and phytopathogenicity
                                                                                                                                                                                                                                            Spiroplasmataceae;
                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
                                    (bases 1 to 6942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
/gene="T22C8.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="T22C8.t1"
complement(19166. .19249)
/gene="T22C8.t1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted using tRNAscan-SE-1.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SISYDYTVIIOHHPLEVTSERKAYRLNCIYRQQESTLQORINVSDIPSTALQSKNAPK
CRYDYLSGSLNGPVVRFANVGDVVVHKWTCDSDREFFVVHSCVYRDESGKDEQEIDER
GCVTDFSLEPEDVSYSDDLKSAFTAVRAFRYADQWNHFSCQITTCQKQENGCEGISP
ICRPMDLGPIKVHYVKHEKNGEKFDEGGGVETLPPRTENTSEGSTTTVRSTTTRERAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="N-terminal portion of this predicted gene show
strong similarity to C. elegans cuticulin"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(19166. .19249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFSTTTHKTTTSSSLQLKTVQRDEDVSNLESFLELSGTFGEVQRLSDETRDRKILKPR
TSPPLWRNNSFSPSSKFRNGYNFPNVESGEGVGQDNTAEFGVKRKSSDAGVNEYGIEI
AKDESQAKONKISLVAEPEKLPKREVFHVETISKTMDSELEPLPYPTKASVYQHRSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="Sptrembl:Q22680"
/translation="MTFVNCFMIIIFVVKNVIADNSNYNFYYTHMEPPKLECGSEGIR
LHINPTGTFGGHVYVRGFFPQTVCHLNYCTRLTNRPIVMDLPFRGPCNVRRRRNVAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="TAA Leu L-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(17992..18093,18136..18440,18799
19407..19781,19822..19987,20032..20250,20393.
20583..20679,20990..21078,21416..21523))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPSMKAAKRRDIHAAHDENSEQKPVRYRALSAEEVRILQTKCARVGPLVOKHCQPKKT
SARNAGRCAAYFRDCAQFIEKGDPLGAIANSFDSGVNINLANVDVKGIPYYPLNEEGA
VGVGVGLGIPFGAWGGGASTSVGVRDYFHGDQEVGANWYDGKYGYKNHWNIPLVQSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLTTLGVLQVISILALITQRFYYKKSIDNLIYADDRPGSRKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHKRVLEDANITLEVETTKIMILENEPSAEKFRLGEAREQSGPEPMKCTTSENYVSNT
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/db_xref="GI:3880003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGAGFQTGQAVAFPGLDVWERALG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGGQHNTVSFPLHGKDAGNLKVDNGYGVGGYYQQNDHVGVNYKEGDVRHTFGVSSPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="SPTREMBL:Q22679"
                                                                                                                                                                                                                                                                                                                               citri.
                                                                                                                                                                                                                                                                                                                                                                                                   GI:17981532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.0%;
Joel, R., Bove, J.M. and Garnier, M.
                                                                                                                                                                                                                                            Spiroplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46.8; [
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Direct Submission

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FEATURES
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Submitted (16-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: zface@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 19, 2002 this sequence version replaced gi:21738685. AL772373 229420 bp Danio rerio clone CH211-143A22, \*\*\* Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads Consensus quality: 218244 bases at least Q40 Consensus quality: 221659 bases at least Q30 Consensus quality: 224352 bases at least Q20 Center: Wellcome Trust Sanger Institute Burton, J.
Direct Submission Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 229420) Danio rerio. Danio rerio Center project name: zC143A22 Web site: http://www.sanger.ac.uk Contact: zface@sanger.ac.uk HTG; HTGS\_PHASE1; HTGS\_DRAFT AL772373.5 GI:21911694 unordered ----- Summary Statistics pieces Genome Center Project Information sum-of-contigs DNA DNA linear HTG 17-JUL-2002 SEQUENCING IN PROGRESS \*\*\*, 23

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Insert size: 162508; 20.8% error; agarose-fp Quality coverage: 6.09x in Q20 bases; sum-of-contigs Quality coverage: 10.15x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13654 136753; gap of 100 bp 10 length 140569 140668; gap of 100 bb 140666 148965; contig of 8197 bp in length 140669 148865; contig of 8197 bp in length 14866 148965; gap of 100 bp 151194 151293; gap of 100 bp 151194 151293; gap of 100 bp 151294 153798; contig of 2505 bp in length 151399 156506; contig of 2505 bp in length 156507 156606; gap of 100 bp 155607 159528; contig of 2608 bp in length 159529 159628; gap of 100 bp 159629 161885; contig of 2022 bp in length 16186 161785; gap of 100 bp 161786 167782; gap of 100 bp 161786 167782; gap of 100 bp 161783 170032; contig of 2057 bp in length 167183 170132; gap of 100 bp 161793 170132; gap of 100 bp 1617933 170132; gap of 100 bp 1617934 172293; gap of 100 bp 1617934 172293;
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location,
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229420: contig of
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ORIGIN
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Best Local Similarity
Matches 119; Conserv
93934 ATTT 93931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94174 AGGAGACATGCGAGTTTCCGGGAGATTATCATTTGCGGGCATCCGAGAGTCTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94114 CATTTGCGGGATACTCCTAGTCTTAGCAACTGGATGAATGTAAAGGAGGACTGCTTCTAC
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                                                                     CGTT 1136
                                                                                                                                               ATAATGGACAACCTGTAATACTTGCTGCAGTACAAAATGGAATCTGCATGTCACCATTTG 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAAC 1012
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                                                                                                                                                                                                                         GCTTCTCAATGTTTATGGGTTTAAGCATTGCATTGATTGCTGCCGTCATTATTACCATTT 1132
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ilarity 48.8%;
Conservative
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225225. .227236
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222633. .225124
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172294. .222532
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fragment_chain:3"
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167283. .170032
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159629. .161685
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156607. .159528
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151294. .15379
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fragment_chain:3"
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fragment_chain:2"
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fragment_chain:1"
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/note="assembly_fragment:00175
fragment_chain:1"
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fragment_chain:2"
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fragment_chain:1"
113930 ...131772
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fragment_chain:1"
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Pred. No. 8.4;
0; Mismatches 125; Indels 0
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCUS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                           51904 TAAGGTTCTCTTTATCTGAGGATGCCGATATGTCTAGTTTTTAGCCTATTAGCCAAAGT 51845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
252 TGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTC 311
                                                                                                                                                 192 TAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGT 251
                                                                                                                                                                                                              106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 29, 2001 this sequence version replaced gi:16974043. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= ... 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: _ EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete sequence. AL645495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sections only once, except for a short overlap.
The true right end of clone RP13-472L18 is at 81091 in this sequence. The true right end of clone RP11-427013 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP13-472L18 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/HGP/Chr13
RP13-472L18 is from the library RPCI-13.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL645495.4 GI:17154392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL645495 81091 bp DNA linear PRI Human DNA sequence from clone RP13-472L18 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-13.2"
a 14138 c 14152 g 25889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="13"
/clone="RP13-472L18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is not the entire insert of clone
                                                                                                                                                                                                                                         3.7%;
                                                                                                                                                                                                           Score 43; DB (
Pred. No. 15;
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TCACCATTCATGGTTTGGTACTGGCCTAACTGGTTTCATAAGCCTAGAATTATTATATGG 51725

Search completed: March 28, 2003, 16:44:58 Job time : 4054 secs

51724 TTAAGGGACTTAAAGACTTTGCTGAGAGCTT 51694

GGAAGCTGATAAAACAGTTAGTGCACAGATT 402

Db Db

51784

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                                                 片
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid concludes a service to identify nucleic acid molecules as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene to therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, and inhibitory compounds of cuticlin may cantibodies raised against it, and inhibitory compounds of cuticlin may call be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of the inminits, or as tools to screen expression libraries to recover desired proteins. They may also be used to target cytotoxic agents to the complement of an open reading frame encoding a cuticlin polypeptide.
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Matches 1161;
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ACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGAT
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                                                                                                                                     Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin protein is useful as a vaccine to prevent parasitic helminth infection
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The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid

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Matches 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecule is useful as a probe to identify nucleic acid molecules, as primer to produce nucleic acids, as a therapeutic reagent, e.g., gentherapy to inhibit cuticlin activity or production, or in a vaccine prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin meall be used in compositions to protect animals, especially mammals as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover desproteins. They may also be used to target cytotoxic agents to the parasite and kill it directly. The present sequence encodes a cuticle polypeeride.
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                              ACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGA
                                                                                                     AAATATGCGGATCGATAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAA
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                                                                                 Claim 1; Page 18-19;
                                                                                                  New parasitic helminth cuticlin proteins and nucleic acids isolated form Dirofilaria immitis, useful for protecting animals from diseases caused by parasitic helminths or for inhibiting molting of filariid larvae in an animal -
                                                                                                                                                             Chandrashekar R,
                                                                                                                                                                                                                                                                                                                  Dirofilaria
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an animal
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                                                                                                                                                                                                                                                                      also
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The present sequence is the coding strand of cDNA encoding novel Dirofilaria immitis cuticlin DiCut-1A protein (see ABP76278). Nucleic acids comprising the complementary strand, the coding sequence coding strand and its complementary strand are also claimed. DiCut-1A cDNA was identified from a D. immitis larval expressed sequence tag DNA sequence on the basis of homology to Ascaris and Caenorhabditis elegans cut-1 cuticlin genes. The encoded protein has 91% identity with the Ascaris homologue. The invention provides D. immitis and Brugia malayi parasitic helminth cuticlin proteins, nucleic acids, antibodies, compounds that

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Best Local :
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(MORA/)
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DB; AAB84259.
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in is useful as
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MORALES T H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morales
                                                                                                                                                                                                                                                                                                                       molecule encoding a Dirofilaria immitis cuticlin as a vaccine to prevent parasitic helminth infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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that encodes a cuticlin protein. The Dirofilaria immilis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin manall be used in compositions to protect animals, especially mammals su as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of

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The specification describes a Dirofilaria immitis nucleic that encodes a cuticlin protein who picage.

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Example 1; Column 43-44;

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                                                                                                                                                                                                                            GGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA
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AAATCTGG
                     AAAACAGG
                                            GAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTT
                                                                                                  TACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAA
                                                                                                                                   GATGATGGAAAAGGTGATGCAGTGGAGATTCTGAATGAAGAAGGATGTGCTTTGGACAAA
                                                                                                                                                                                                                                                                           GGTGGACCAACTGGTGCACCTGTTCGATTTGCAATGATTGGAGATCATGTATATCACAAA
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 879
                     845
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76.98;
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.19-JUN-2001
                                                                                                                               01-JUN-1998;
                                                                                                                                       01-JUN-1999;
                                                                                                                                                                Dirofilaria
                                                                                                                                                                         Cuticlin; gene therapy; vaccine;
                                                                                        Novel
                                                                                                        Chandrashekar R, Morales
                                                                                                                                                        US6248329-B1
                                                                                                                 (CHAN/) CHANDRASHEKAR (MORA/) MORALES T H.
                                                                                                                                                                                          22-AUG-2001
                                                                                                                                                                                                            AAH24831 standard; DNA; 1372
                                                                                                                                                                                 sequence
                                                                                                                                                                                          (first
                                                                                                                              98US-0087435
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                                                                                                                                                                                 of
                                                                                                                                                                                          entry)
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                                                                                                                                                                                                            ВP
                                                                                                                                                                        helminth parasite;
                                                                                                                                                                                  strand
                                                                                                                                                                                  of.
                                                                                                                                                                                  cuticlin
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protein nucleic acid molecule encoding a Dirofilaria immitis cuticlin in is useful as a vaccine to prevent parasitic helminth infect infection

Example 1; Column 43-46; 29pp; English.

The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid molecules is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin may all be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover desired proteins. They may also be used to target cytotoxic agents to the parasite and kill it directly. The present sequence represents the complement of DNA encoding a cuticlin polypeptide.

Sequence 1372 BP; 406 A; 281 C; 229 G; 456 T; 0 other;

Similarity

43.48;

DB 22;

Length

В Ş Š 밁 Š Qy 밁 밁 δÃ Query Match Best Local Sin Matches 652; 1101 1341 1281 60 1 ATGATGATTCGTCTTATTGCTTTCTGTACTCACACTTATTG-CATTGTCTTATTCGATTCC CAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCA TATTGACAATGGTGTCGAAGGTGAACCTGAAATAGAATGTGGCGCAGCTTCGATAACAAT GGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAAT ATTATCATTATTCTCCTTGTTATTCCTACTTTTCTACTTGACCTACGTATCATCGATCCC GGATGAATGTCGTTCAGATAGTAATGGACGGCAGGTAGCTGGAATCGAATTGGCAATGGA AGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCCGGAATTTCACTTCCATTTGA CAATTTCAATACTAGAAATACATTTGAAGGACACGTATATGTAAAAGGACTCTATGATCA Conservative Score 504.2; Pred. No. 2.5e 0; Mismatches 0; ω •• Gaps 1042 1222 1282 59 ω --

RESULT 7 AAH24831/c

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RESULT 8
ABL57373
ID ABL5
XX ABL5
XX ABL5
XX CL1
AC Dirc
XX Cuti
KW Cuti
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  (CHAN/) CHANDRASHEKAR
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                                                                                                                                                                              US2002037294-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dirofilaria
                                                                                     20-MAR-2001;
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htic; gene;
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                                           99US-0323427
                                                                                                                                                                                                                                                                                                             Location/Qualifiers 392..1207
                                                                                                                                                                                                                      /product= "DiCut-1B"
/note= "the CDS is a
Claim 1"
                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cdna;
                                                                                                                                                                                                                                                                                                                                                                                                                         parasite; DiCut-1B; vaccine; gene therapy;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention provides D. immitis and Brugia malayi parasitic helmint: cuticlin proteins, nucleic acids, antibodies, compounds that inhibit cuticlin activity, and methods of obtaining them.
Therapeutic compositions comprising such proteins, nucleic acids, antibodies and/or inhibitors, including genetic vaccines, recombinant virus vaccines and recombinant cell vaccines, are use to protect animals from diseases caused by parasitic helminths, at to inhibit the moulting of filariid larvae in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dirofilaria immitis cuticlin DiCut-1B protein (see ABB76279). Nucleic acids comprising the complementary strand, the coding sequence coding strand and its complementary strand are also claimed. DiCut-1B cDNA was identified from a D. immitis larval expressed sequence tag DNA sequence on the basis of homology to Ascaris and Caenorhabditis elegans cut-1 cuticlin genes. The encoded protein has 81% identity with the Ascaris homologue. The invention provides D. immitis and Brugia malayi parasitic helminth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New parasitic helminth cuticlin proteins and nucleic acids isolated form Dirofilaria immitis, useful for protecting animals from diseases caused by parasitic helminths or for inhibiting molting of filariid larvae in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1372 BP; 456 A; 229 C; 281 G;
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Dirofilaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 23; 32pp;
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GGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAA
                                                                   ACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGAT 477
                                                                                                                                           ATGCTTTTACATGG-AAGCTGATAAAACAGTTAGTGC-ACAGATTGAGGTATCTGAAATC
                                                                                                                                                                                          TGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACA
                                                                                                                                                                                                                                                                    TTCGTGTAATGTTGAACGATCACGATCCTTAAATCCTCGTGGTGTTTTTGTAACAACTGT
                                                                                                                                                                                                                                                                                                                                          GGATGAATGTCAGATAGTAATGGACGGCAGGTAGCTGGAATCGAATTGGCAATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTGACAATGGTGTCGAAGGTGAACCTGAAATAGAATGTGGCGCAGCTTCGATAACAAT
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                                                                                                                      ATGTTTTTATATGGAAAGCTGATAAGACCGTTAGTACTGGTCCTTGAAGTATCTGAAATG
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                                                 ACTACAGCATTCCAAACTCAAGTGGTACCAATGCCCGTATGTCGATATGAGATTTTGGAA
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DB; ABB76279.
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Pred. No. 2.5e-131;
0; Mismatches 193;
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that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein,
                                                                                                                                                                                                                                                   Novel nucleic acid
protein is useful
                                                                                                                                                                                                                                                                                                                                                                                                      Chandrashekar R,
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                                                                                                                                                                             Disclosure;
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MORALES T H.
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/product= "cuticlin"
/note= "no termination"
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158..892
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                                                                                                                                                                                                                                                d molecule encoding a Dirofilaria immitis cuticlin as a vaccine to prevent parasitic helminth infection
                                                                                                                      describes a Dirofilaria immitis nucleic acid molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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RESULT 10
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AC AAH24
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standard;

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22-AUG-2001 AAH24840; AAH24840

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 892
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                                               TAATTTAATTAATGAAGAAGGATGTGCATTAGATCGATATCTTCTAAATAATTTGGAATA
                                                                                                          TGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGT
                                                                                                                                             CCAGTATGCTAATATTGGACAACCGGTTTATCATAAATGGACATGTGATTCTGAAACCAGT
                                                                                                                                                      TCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTGAAGGACATGTATATGCTAAAGGATTATACAGTAATCAAGATTGTCGTAGTGATGA
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TCCAACTGATCTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCG
                                                                                               TGATACCTTCTGTGCTTTGGTACATTCCTGTTTTGTTGATGATGGCAATGGTGACAGTAT
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78.1%;
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Pred. No. 2.8e-119;
0; Mismatches 155;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuttclin protein. The Dirofilaria immitis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin may all be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover desired parasite and kill it directly. The present sequence is the complement
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 892 BP; 292 A; 168 C; 142 G; 290 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin protein is useful as a vaccine to prevent parasitic helminth infect:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chandrashekar R,
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(MORA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 55-56; 29pp; English.
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                                                                                                                                                                                                                                                                    TTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGG
                                                          ATTATTTGTTACCAAAGTTGATCGTGCATATCGACTACAATGCTTTTACATGGAAGCTGA
                                                                                                                                                                                                              TTTTGAAGGACATGTATATGCTAAAGGATTATACAGTAATCAAGATTGTCGTAGTGATGA
                                          ACAGTTTATCACAAAAGTTGATCGAACATATCGATTGCAATGCTTTTACATGGAAGCTGA
                                                                                                               ACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCC
                                                                                                                                                        AGGTGGACGTCAGGTAGCCGGAATATCATTACCGTTTGATTCATGTAATGTCGCACGTAC
                                                                                                                                                                     AGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTAC
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                                                                                                ACGTTCGTTAAATCCACGTGGAATATTTGTCACAGCTGTTGTGGTAATTACGTTTCATCC
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                                                                                                                                                                                                                                                                                                                                                                                   554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 open reading frame encoding a cuticlin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 2.8e-119;
0; Mismatches 155;
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No. 2.
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RESULT 11
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                                                                                                                                                                                   New parasitic helminth cuticlin proteins and nucleic acids isolated form Dirofilaria immitis, useful for protecting animals from diseases caused by parasitic helminths or for inhibiting molting of filariid larvae in an animal -
                                                                                                                                                                                                                                                                                                               P-PSDB;
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                                                                                                                                                                                                                                                                                                               ABB76280
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tic; gene;
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/partial
/note= "the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0323427
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ds.
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The present sequence is the coding strand of a partial cDNA clone for novel Brugia malayi BmCut-1B protein (see ABB76280). The complementary strand of this sequence is also claimed. The BmCut-1A cDNA was obtained from adult female cDNA by PCR

using primers

Dirofilaria

Claim

9;

Page

32pp;

English

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RESULT 12
AAH24832
ID AAH24
XX
AC AAH24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cuticlin nucleic acids. The invention provides D. immitis and B. malayi parasitic helminth cuticlin proteins, nucleic acids, antibodies, compounds that inhibit cuticlin activity, and methods of obtaining them. Therapeutic compositions comprising such proteins, nucleic acids, antibodies and/or inhibitors, including genetic vaccines, recombinant virus vaccines and recombinant cell vaccines, are used to protect animals from diseases caused by parasitic helminths, and to inhibit the moulting of filariid larvae
              22-AUG-2001
                                                                      AAH24832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                         TCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAAT
                                                                                                                                                                                                                                                                                                                               TCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGT
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                                                                                                                                                                                                                     GGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTATTTGGAATA
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                                                                                                                                              TCCAACTGATCTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCG
                                                                                                                                                                                                   TAATTTAATTAATGAAGAAGGATGTGCATTAGATCGATATCTTCTAAATAATTTGGAATA
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                                                                      DNA;
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78.1%;
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Pred. No. 2.8e-119;
0; Mismatches 155;
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GTGATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATA

CAGAGACTACAGATACATTCTGTGCATTAGTACATTCATGTGTTGTGGGATGATGGAAAAG

CTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACG GTGCACCTGTTCGATTTGCAATGATTGGAGATCATGTATATCACAAATGGACATGTGATT γ

372 GGAAGCTGATAAAACAGTTAGTGC-ACAGATTGAGGTATCTGAAATCACAACTGCTTTTC 430

GAAAGCTGATAAGACCGTTAGTACTGGTCCTTGAAGTATCTGAAATGACTACAGCATTCC

73

AAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCG 490

AAACTCAAGTGGTACCAATGCCCGTATGTCGATATGAGATTTTGGAAGGTGGACCAACTG

GTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGGGACATGCGATT 550

193

Matches 455; Query Match

Local

Similarity

26.7%; 70.7%;

Score 310.4; Pred. No. 5.9

Conservative

0

Mismatches 161;

Indels Length

28;

Gaps

2

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.9e-77 DB 22;

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14

431

491 74

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molecule is useful as a probe to identify nucleic acid molecules, as primer to produce nucleic acids; as a therapeutic reagent, e.g., gen therapy to inhibit cuttclin activity or production, or in a vaccine prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin me all be used in compositions to protect animals, especially mammals as as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover des proteins. They may also be used to target cytotoxic agents to the parasite and kill it directly. The present sequence encodes a cuticle
                                                                                                                                                                                                                                                                                                                                                                                (CHAN/)
(MORA/)
  Sequence
                                                                                                                                                                                                     The specification describes a Dirofilaria immitis nucleic acid
                                                                                                                                                                                                                                 Example 1; Column 45-48;
                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin
                                                                                                                                                                                                                                                                                                                                                       Chandrashekar R, Morales
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6248329-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuticlin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a cuticlin polypeptide
                            polypeptide.
                                                                                                                                                                                          encodes a cuticlin protein.
                                                                                                                                                                                                                                                                                                                                                                                CHANDRASHEKAR R. MORALES T H.
  813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immitis
  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0087435
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1..813
  247
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 A; 148 C; 164 G;
                                                                                                                                                                                                                                                                        a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; helminth parasite;
                                                                                                                                                                                                                                29pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cuticlin"
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                                                                                                                                                                                          The Dirofilaria immitis nucleic
                                                                                                                                                                                                                                                                       prevent parasitic helminth
254 T; 0 other;
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                                                                                                                                                                                                                                                                       infection
                                          cuticlin
                                                                                                                                                                                                      molecule
                                                                   desired
                                                                                                                                                               gene
                                                                                                                                                                            as a
                                                                                                          such
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SSSSS

parasite and of an open re

proteins. They may also be used to target cytotoxic agents parasite and kill it directly. The present sequence is the

ite and kill it directly. The present sequence is the open reading frame encoding a cuticlin polypeptide.

complement to the

BP; 254 A; 164 C; 148

G; 247 T; 0 other;

2

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RESULT 13
AAH24833/c
ID AAH248
XX AAH248
XX Nucleo
XX Cuticl
XX Cuticl
XX US6248
XX US6248
YX US6248
YX O1-JUN
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                The specification describes a Dirofilaria immitis nucleic acid molecule that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin may all be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of
                                                                                                                                                                                                                                                                                                                            Example 1; Column 49-50;
                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin protein is useful as a vaccine to prevent parasitic helminth infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681
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WO9807830-A2

Methanococcus

jannaschii.

Methanococcus jannas
genome; autotrophic;

jannaschii; methanogenic

extrachromosomal

element; archaeon;

i; circular chro
identification;

Methanococcus 10-NOV-1998

jannaschii circular

chromosome

(first entry)

AAV21209;

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RESULT 15
ABL32426/c
ID ABL32426 standard; D
XX
AC ABL32426;
XX
DT 26-MAR-2002 (first
XX
DE Human immune system
XX
KW Human; immune system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the complete 1.66-megabase pair genome sequence of the Methanococcus jannaschii circular chromosome. The present invention describes M. jannaschii open reading frames from the genome sequence. The invention also describes a computer based system for identifying fragments of the M. jannaschii genome that are chomologous to target nucleotide sequences, comprising: (a) data storage means comprising the nucleotide sequence of the 164976, 58407 or 16550 bp sequence (see AAV21209, AAV21210 and AAV21211), or a nucleotide sequence of the sequence of the sequence of the data storage means to carget sequence to the nucleotide sequence of the data storage means to identify a homologous sequence, and (c) retrieval means for obtaining the homologous sequence. The method, which is based on whole genome crandom sequencing of an autotrophic archaeon M. jannaschii, the genome composition of the 164976 bp sequence given in AAV21210), and a small circular extra-chromosomal element (the 16550 bp sequence given in AAV21211), can be used in the identification of M. jannaschii genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                      684746 CTGAATTGAGCTGTTGGTGACTTTGCAGGCAATCCGAGTTTTTCCTCTCAACTCAACAATC 684687
                                                                                                                                                                                                                                                                                                                                                                                                                                           684806 ATTAATTTATCAAATTTTAACTCTTTAATTAATGTTCTAACTTCTTCCAAATCCTTCTCA 684747
                                                                                                                                                                                                                                 684626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-)
                                      Human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1664976 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 152-585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of methano-genic jannaschii - useful in identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                           727
                                                                                                                                                                                                                               GCTAATGCCATATTTCCTTTTTGAGCGGCAATATTTCTTAAAGTTTTTATGATTTCTGTA 684567
                                                                                                                                                                                                                                                                GGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCA 906
                                                                                                                                                                                                                                                                                                     TGGTTATTTGCAGGAACAGCATGTCCAAATCTTAAAACATAAGAAGCTGTTTTTCTATGT
                                                                                                                                                                                                                                                                                                                                                                                                       GCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAAT 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATAT 726
                                                                                                                                                                                                                                                                                                                                     AGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGT 846
     immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith HO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENOMIC RES.
ILLINOIS FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOHNS HOPKINS SCHOOL MEDICINE
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US14900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.48;
47.98;
                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    568133 A; 264649 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614pp; English
                                                                                                                                            9810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 20;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
                                      gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White OR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258701 G; 573392 T; 101 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           archaeon, Methanoccoccus
M. jannaschii genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Woese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1664976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 16
AAX99556/
SEXEXEX
EXSXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                   5409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders including eye diseases such as retinopathy, neocatar glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelol leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                           5229
                                                                                                                                                                                                             5289
                                                                                                                                                                                                                                                                5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; a acute myeloid leukaemia; Alzheimer's disease; AIDS; epilep
                                     05-OCT-1999
                                                              AAX99556;
                                                                                      AAX99556
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9810 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                  831 AGCTGTTAAAACA 843
                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                TCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTAC 770
                                                                                                                                                                                                                                                                                                                   CATTAAAGAACCAAATAGCGAATGTTCGACCACAATGTTCAGAACCACAAGGATTCGG
                                                                                                                                                                                                                                                                ATAAAAAAAAAAACATACGTATCTTAAAAATCTTTAACCAAACAATTTCTATTTTAA 5290
                                                                                                                                                         AACTAACAAAACA 5217
                                                                                                                                                                                                                                                                                                                                                                        . Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                      standard; DNA; 14066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 399; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1032529
2000DE-1043826
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             2770 A; 79 C; 1978 G; 4983 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG
                                                                                                                                                                                                                                                                                                                                                                                   3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin
                                                                                                                                                                                                                                                                                                                                                                      Score 39.4; DI
Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                  DΒ
                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene, us
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaemia;
                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0;

Nucleic acid

sequence from U.

urealyticum

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RESULT 17
ABK39779/c
ID ABK397
XX ABK397
AC ABK397
XX
DT 21-MAY
XX
DE CDNA e
XX
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                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                    Query Match
          cDNA encoding full length L1428P
                                          21-MAY-2002
                                                                       ABK39779;
                                                                                             ABK39779 standard; cDNA;
                                                                                                                                                                                                                                                                           forming target:probe complex is copmplementary to a region selected from one of the 181 nucleic acid sequences (AAX99501-681). U. urealyticum is an opportunistic pathogen of the human urogenital tract that is a significant cause of adverse pregnancy outcome, neonatal disease, and suppurative arthritis. As the infections are commonly asymptomatic, it is presence in a patient. Also, as the pathogen has no current antibiotic directed specifically against it, it would be advantageous to isolate and basis for diagnosis of U. urealyticum infection as well as to develop new and improved drug therapies. The present invention provides such novel polynucleotide sequences (AAX99501-681).
                                                                                                                                                                     9076 AG
                                                                                                                                                                                                                  9136 TATTAAAACAGTTAGTGCACATAATGCTCAAGTACATTTTAAGCTTAAAACAAATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14066 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AAX99501-081) that can be used in the method of the invention by sample. The probes that can be used in the method of the invention by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides methods for the detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 41-46; 110pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of Ureaplasma urealyticum using
                                                                                                                                                                                                 201
                                                                                                                                                                                                                                              141 ATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-469343/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cassell GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ureaplasma urealyticum; nucleic acid detection; infection; pathogen; human urogenital tract; pregnancy; neonatal disease; drug therapy; suppurative arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lefkowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9939007-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                           81 TGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAATCTAATATATAATACACGTAATGC 140
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                 Ą
                                                                                                                                                                                                                                                                                                                                        70;
                                                                                                                                                                     9075
                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                     3.3%;
ilarity 57.4%;
Conservative
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen EY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0073189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US01972
                                                                                                                                                                                                                                                                                                                                                                                        4508 A; 1702 C; 1539 G; 6317 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glass
                                                                                              6799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection. It provides novel genes used as a source of primers and probes for the
                                                                                                                                                                                                                                                                                                                                     Score 38.8; D
Pred. No. 4.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glass JS,
                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel
                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes, probes
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                              Length 14066;
                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                 Gaps
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EX DX AX
                                                                                                                              ABQ70961/c
ID ABQ70961 standard; DNA; 6242
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein fragment, described in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from utton at the sequence and of the sequence of the printed specification, but was obtained in electronic format directly from utton at the sequence and the sequence of the printed specification, but was obtained in electronic format directly from utton at the sequence and the sequence of the seque
                                                                                                                                                                                                                                                       4942
                                                                                                                                                                                                                                                                                                                                               5002
                                                                                       ABQ70961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6799 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2000;
29-AUG-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                             235 TTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 1883; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-164634/21.
P-PSDB; AAU85654, AAU85655, AAU85656, AAU85657, AAU85658, AAU85659
                                                                                                                                                                                                                                                                                               295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T, Watanabe Y, Henderson RA, John:
Marnerakis M, Carter D, Fanger GR, Ved
Mcnabb A, Wang A, Fanger N, Switzer A,
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13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2002
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cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                         GTACCTGTGCTGACTTTATTTCCTAGATGATTTATTCCTTTATTTTATGG
                                                                                                                                                                                                                                                                     ACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCG
                                                                                                                                                                                                                                                                                                                                 TTTGTTACAAGCAAAATCGGAGTCCCACGGAGTCTCAATCGCCATGGTGTTTCTCTGTCA 4943
                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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2000US-0651563.

; 2000US-0658824.

; 2000US-0671325.

; 2000US-0677419.

; 2000US-0702705.

; 2000US-0736457.

; 2001US-0849626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1801 A; 1865 C; 1539 G; 1594 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 24; Pred. No. 5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson JC, Re
, Vedvick TS, I
zer A, Mcneill
                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bangur CS;
PD, Clapper JD;
                                                                                                                                                                                                                                           4893
                                                                                                                                                                                                                                                                                          344
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Listeria monocytogenes 4b contig DNA sequence #903

29-AUG-2002

(first entry)

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RESULT 19
AAZI6979/c
ID AAZI69
XX AZI69
XC AAZI69
XY 12-OCT
XX
DE Human
XX
KW Human;
KW detect
KW geneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP )
            Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                    3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators \,
                                                                                                                                                                   AAZ16979 standard; cDNA; 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; infection; ds.
                                                                                                          12-OCT-1999
                                                                                                                                                                                                                                              3052 AAGTAACCTCTGAAGTTGGTGTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6242 BP; 1954 A; 1060 C; 1164 G; 2064 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000; 2000FR-0012697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2001; 2001WO-FR03061.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listeria
                                                                                                                                                                                                                                                                                                                          881 TTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATA
                                                                                                                                                                                                                                                                                                                                                                                                821 AAGGATTCGGAGCTGTTAAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                        TCAACACCCTTGAAATTAGCGATGAT 966
                                                                                                                                                                                                                                                                                                      TTATTTAATGTCGAAAGAAAAGGCAGTCGCGGAAAACATTCCTTATATCGCAACAATCA 3053
                                                                                                                                                                                                                                                                                                                                                                AAGAAGGTGGAACGGTTACAGCCGGCAATGCTTCCGGTATCAATGATGGAGCTTCCGCAA 3113
                                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INST PASTEUR.
CNRS CENT NAT RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections by Listeria, and are useful as immunogens in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocytogenes 4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glaser P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 3774; 180pp; French.
                                                                          expression
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria;
                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%;
                                                                          product cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37.2; D
Pred. No. 9.3;
                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DΒ
                                                                          SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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                                                                          IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                          NO:4449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6242;
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
               SS
                                                                                                                                                                                                                                                                                                                                      940
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                                                                                                                                                                                                                                                             CC comprising the sequences given in AAZI2532 to AAZI779. Also described is CC cancerous state of a mammalian cell, comprising the sequences given in AAZI2532 to AAZI7799. Also described is CC a method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell CC suspected of being cancerous, where the gene product is encoded by one CC plynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides CC can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct CC arrays for diagnostics (which may be used to determine function of an CC encoded protein); and to detect differences in expression levels between CC identify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC diagnosis, prognosis and management of colorectal cancer, breast cancer, CC and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1998;
28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escobedo J, García PD, García V, Giese K, Inn
Jones WL, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 2107; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human genes and their expression products which differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crkvenjakov R,
Escobedo J, G
                                                                                                                                                                                                                                                         Sequence 783 BP; 243 A; 176 C; 145 G; 197 T; 22 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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 272
                                708
                                                                                                                                392
                                                                                                                                                           Local
                                                                                 1999-494092/41.
GGGTCCTGTTTATCCATTTGCTTCTTGAT
                                AGCTCACGTATACAAATATGCGGATCGAT 736
                                                                AGTTTCACAATATGTGATCTATTACTTGATATAACCCATTGCAGTAAGGGATGAGCAAGG
                                                                                                                            CTGCTGAGAAGAAGGAACTGATGTGGAGTATGCATAAACTTCAATTGCCTGTTAACTGGC
                                                                                                                                                                                             79;
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                         analogues
                                                                                                                                                                                             Conservative
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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                                                                                                                                                                                                                                                                                         and antagonists.
                                                                                                                                                                                                          3.2%;
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                                                                                                                                                                                         Score 37; DB 2
Pred. No. 4.1;
0; Mismatches
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'V Innis !
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                                                                                                                                                                                             0,
                                                                                                                                                                                           Gaps
                                                                                                                            333
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RESULT 20 AAX99054/c

0;

standard;

CDNA;

ВP

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CC proteins, 7 transmembrane receptors, ATPases associated with various C cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of C transcription factors, G-protein alpha subunit, phorbolesters or CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, CC protein tyrosine phosphatase, trypsin, wnt family of developmental CC signalling proteins and WW/rsp5/WWP domain containing proteins. The CC encoded polypeptides also have a functional domain selected from Ank CC repeat, basic region plus leucine zipper transcription factors, CC bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CCHC class), and zinc-binding metalloprotease (C domain. The polynucleotides encode polypeptides with similarity to known protein families and are predicted to have similar properties. The novel CC applications. In particular, the products for use as therapeutic agents and in forensics, genetic analysis, mapping and diagnostic can be used for treating e.g. cervical CC cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas, celoretinoblastoma, myosarcomas, lung carcinomas, leukemias, such as Chronic myelogenous leukemia, promyelocytic leukemia, and drift can be used for treating e.g. cervical complications and lymphomas such as histiocytic lymphoma, anhydric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-DEC-1998;
23-DEC-1997;
03-APR-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by screening for differential expression in colon cancer, breast cancer and lung cancer cell lines. The polynucleotides of the invention are represented in AAX98275-X99118 and encode polypeptides of protein families selected from 4 transmembrane segments integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamson G, Le
Stache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escobedo J,
Jones LW, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ov R, Dickson M, Drmanac R, Drmanac S;
J, Garcia PD, Garcia V, Giese K, Inni
Kassam A, Kennedy GC, Kita D, Labat
Leshkowitz D, Pot D, Randazzo F, Rei
in B, Sudduth-Klinger J, Williams LT;
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31-MAR-1998;
03-APR-1998;
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(HYSE-)
                                                                                                                                                                                                                                                   Escobedo J. Garcia PD. Garcia V. Giese K.
Jones WL. Kassam A. Kennedy GC. Kita D. La
Lamson G. Leshkowitz D. Pot D. Randazzo F.
Stache-Crain B. Sudduth-Klinger J. Williams
                                                                                                                                                                                                                                                                                                                                         Crkvenjakov R,
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AAZ17515
                                                                                                                                              Novel human genes and their differentially expressed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCTTTGTCGATGATGGTAAACGGTGATACTGTGGAAATTCTAAATGCTGATGGGTGC
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ion; mapping; tissue typing; profiling; foren
c analysis; colorectal cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                  CHIRON CORP
HYSEQ INC.
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98US-0072910.
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                                                                                                                                                                                                                                                                                i, Drmanac R, Ulum. Innis
                                                                                                                                              expression different (
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forensic; cancer;
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the

expressed genes correlated wit comprising detecting at least

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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23-DEC-1997;
03-APR-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer; human; colon; breast; lung; transmembrane receptor; ATPase; integral membrane protein; aspartyl protease; GAPA family; wnt family; transcription factor; G-protein alpha subunit; protein phosphatase; phorbolester binding protein; diacylglycerol binding protein; trypsin; protein kinase; tyrosine phosphatase; developmental signalling protein; ww/rsspS/wwp domain; therapy forensic; genetic mapping; diagnostic; detection; treatment; cervical; melanoma; colorectal adenocarcinoma; wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
                                                                                                                                                                                                                                                                                                                  08-JUL-1999
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                                                                                                                                                                                                                                                     22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide analogues and antagonists.
   (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTCCTGTTTATCCATTTGCTTCTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTCACGTATACAAATATGCGGATCGAT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGTTTCACAATATGTGATCTATTACTTGATATAACCCATTGCAGTAAGGGATGAGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTGAGAAGGAACTGATGTGGAGTATGCATAAACTTCAATTGCCTGTTAACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphoma; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                       98US-0217471.
97US-0068755.
98US-0080664.
98US-0105234.
                                                                                                                                                                                                                                                     98WO-US27610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 A; 186 C; 143 G; 208 T; 30 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA; 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocore 37; DB
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647
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RESULT 23
AAC79937/c
ID AAC79937 standard; cDNA; 1/
XX
AC AAC79937;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human secreted protein enco

Human secreted protein encoding cDNA for gene 40.

(first entry)

밁 δÃ 멍 δÃ 밁 Ş

257 GGGTCCTGTTTATCCATTTGCTTCTTGAT

229

AGCTCACGTATACAAATATGCGGATCGAT

AGTTTCACAATATGTGATCTATTACTTGATATAACCCATTGCAGTAAGGGATGAGCAAGG

258

CTGCTGAGAAGAAGGAACTGATGTGGAGTATGCATAAACTTCAATTGCCTGTTAACTGGC

318

Matches Query Match

Local

Similarity

3.2%; 53.0%;

pred. No. 4.1; 0; Mismatches

70;

0

Gaps

0

Conservative

Sequence 795

B₽;

228 A; 186 C; 143 G;

208

T; 30 20;

other; Length 795 Indels

of.

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CC protein tyrosine phosphatase, trypsin, whit family of developmental CC signalling proteins and WW/rsp5/WWP domain containing proteins. The CC encoded polypeptides also have a functional domain selected from Ank CC repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (CCHC class), and zinc-binding metalloprotease commain. The polynucleotides encode polypeptides with similarity to known protein families and are predicted to have similar properties. The novel polynucleotides can be used to develop products for use as therapeutic cagents and in forensics, genetic analysis, mapping and diagnostic capents and in forensics, spentic analysis, mapping and diagnostic cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas, convectinoblastoma, myosarcomas, lung carcinomas, Wilm's tumour, sarcomas, retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic myelogenous leukemia, and lymphomas such as histiocytic leukemia, and compenital dysplasia, congenital alveolar dysplasia, breach control of the cervix, fibrous dysplasia of bone, and breach condenses and control of the cervix, fibrous dysplasia of bone, and breach condenses are condensed to the cervix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel isolated human polynucleotides obtained by screening for differential expression in colon cancer, breast cancer and lung cancer cell lines. The polynucleotides of the invention are represented in AAX98275-X99118 and encode polypeptides of protein families selected from 4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbolesters or diaryiglycerol binding proteins, protein kinase, protein phosphatase 2C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones LW, Kassam A, Kennedy GC, Kita D, Labat
Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                       mammary dysplasia, l
prostate or thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 453-454; 591pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escobedo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-430243/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dickson M, Drmanac R, Drmar
Ircia PD, Garcia V, Giese K,
                                                                       hyperplasias, e.g. endometrial, adrenal, breast, d hyperplasias or pseudoepitheliomatous hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac S;
Innis )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Labat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinhard C;
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밁 Š 밁 δõ В

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disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. y. conneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides are used to modulate mammalian metabolism, to change mammal's mental state or physical state by influencing biorlythms circadian rhythms, depression tendency for violence tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, stress or other increase or decrease storage capabilities, fat content, lipid, protein, camponare, vitamins, minerals, cofactors or other nutritional
  Query Match
Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies to (II) can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial, virucide, fungicide and ophthalmological activity and which can be used for gene therapy. (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human secretory proteins, nucleic acids encoding them and antibodies directed against them, useful for diagnosing and treating disorders related to the proteins such as cancer, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ophthalmological; gene therapy; treatment; autoimmune disease; infection; cardiovascular disorder; nervous system disorder; ocular disorder; wound healing; epithelial cell proliferation; skin aging; mental state; transplantation; metabolism modulation; ss.
                                                                                     Sequence 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel isolated polypeptide (I) and its encoding nucleic acid molecule (II) which have immunosuppressive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim la; Page 371-372; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB44956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-2000; 2000WO-US06042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200055200-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
nootropic; neuroprotective; antibacterial; virucide; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-656008/63
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0124143.
99US-0168663.
                                                                                     482 A; 288 C;
                  3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; antiarthritic; antirheumatic;
                      Score 37;
Pred. No.
ed. No. 5.5;
Mismatches
                                                                                     292 G;
                                                                                   405 T; 0 other;
                                          DB 21;
                                          Length 1467;
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Conservative

0;

70;

Indels

0;

0

Query Match
Best Local Similarity

Conservative

Score 37; DB Pred. No. 5.5; 0; Mismatches

70;

Indels

0,

Gaps

0

DB

22; Length 1467;

1467

BP;

482 A; 288 3.2%;

Ç

292 G;

405 T; 0 other;

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RESULT 24
AAA33034/c
ID AAA330
XX AAA330
XX AAA330
XX Human;
XX Human;
XX Human;
XX Human;
XX Homo s
YX WO2001
XX 29-SEF
PR 29-SEF
PR 03-NOV
XX WO2001
XX Ruben
DR WPI; 2
DR WPI
                                                                                                                                                                                               inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnos and treatment of colorectal carcinomas and cancers. AAH37196 to AAH3720 and AAB77789 represent sequences used in the exemplification of the
                                                                  N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                      cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon
                                                                                                                                                                           present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAG73603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH33034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH33034 standard; cDNA; 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-235357/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTCACGTATACAAATATGCGGATCGAT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTTTCACAATATGTGATCTATTACTTGATATAACCCATTGCAGTAAGGGATGAGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGAGAAGAAGGAACTGATGTGGAGTATGCATAAACTTCAATTGCCTGTTAACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 2277; 9803pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0157137.
99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birse CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
                                                                                                        sequences are
                                                                                                                                        sequence listing were
                                                                                                        present
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                                                                                                                                                                                                                                                                            diagnosis
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RESULT 25
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Best Local
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and the sequence of th
                                                                             1030
                                                                                                                                                                                                                                                                                                                                                                                                                           anti-Listeria vaccines.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INSP )
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ABQ70472 standard;
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and pathogenicity of Listeria (potential therapeutic agents), treating infections by Listeria, and are useful as immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; SEQ ID 3285; 180pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002
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                                                                                                                                                   . Similarity
82; Conserv
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CNRS CENT NAT
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                            434 A; 339 C; 306 G;
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                                                                                                                                                                                                                     Score 37; DB:
Pred. No. 5.8;
0; Mismatches
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TACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTG 188

Query Match 3.2%; Best Local Similarity 48.1%; Matches 104; Conservative

0;

Mismatches

112; 22;

Indels Length 6571;

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Gaps

0

Score 36.8; Pred. No. 12

12; DB

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AAA89354/c
ID AAA89354 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
                                                  promoter. Transformants were selected and their progeny screened for hygromycin resistance. The mutant phenotype (hygromycin resistance) was screened for genetic co-segragation with a specific T-DNA insert. Cloning of the tagged gene allowed characterization of the present sequence. 2 Allelic differences were found in the corresponding gene of A. thaliana ecotype Columbia (see AAA89385).
                                                                                                                                        hydrogrmycin resistance gene (hyg). Mutation of a silencing modified locus results in release of silencing of the hyg gene and restores hygromycin resistance. Plants homozygous for the silent resistance gene were subjected to transformation with a bar selectable marker gene under control of the T-DNA 1'-2' dual
                                                                                                                                                                                                               The present sequence is that of Arabidopsis thaliana ecotype Zurich epigenetic silencing gene MOM cDNA clone. It encodes a 2001-amino acid protein (see AAB20062) with similarity with ATPase/helicase proteins of the SWIZ/SNF2 family, which controls gene silencing, particularly plant gene silencing. Trans-acting modified loci were identified by T-DNA insertion mutagenesis using Arabidopsis thaliana ecotype Zurich, which carries a heritable inactivated, methylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
Sequence 6571 BP;
                                       Gene silencing is useful as a molecular tool for regulating
                                                                                                                                                                                                                                                                                                                                        Claim 6;
                                                                                                                                                                                                                                                                                                                                                                    Novel gene encoding a protein that controls gene silencing, particular silencing of plant genes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Habu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana silencing gene cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAB20062
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mittelsten Scheid O,
                                                                                                                                                                                                                                                                                                                                     Page 22-32; 48pp; English.
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2060 A; 1347 C; 1470 G;
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1694 T;
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0 other;
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RESULT 27
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ID AA165
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Ph We butt
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FT CDS
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                                                                               Matches
                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                  The present nucleic acid sequence comprises a phage resistance mechanism. Plasmids that contain the phage resistance mechanism nucleic acids are used to impart phage resistance to industrially important strains of lactic acid bacteria. These recombinant strains are then used for preparation of cheese, yogurt, butter, sauces and
                                                                                                                                                                              Sequence 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid for imparting phage resistance to lactic acid bacteria used in food preparation comprises a polynucleotide that encodes a
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 16-17; 30pp; French
phage-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUDD ) SKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phage resistance mechanism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6384 TATATATATATATTATTAACTCTCTAAAAATCA 6349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          743
                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-611505/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGATGTACGAACTGATATCAACACCCTTGAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTATTTATATACATGAAAGTAGAACGTTGCGTTTCAAAAGGAGAGACCTTAGCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTCGGTTCCTGACTCACTAAATTAGATTAACGACAGAGATTAGGTAACCTACTTATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAAC 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTTCGAC
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sauerkraut;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence comprising a phage resistance
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE PROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 272..1456
                                                                                                                                                                                                                                                                                                                                                                                                                                            mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                              612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                              3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                         A; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOLDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1527
                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lactic acid
                                                                                                 Score 36.6;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽P
                                                                        Mismatches 124;
                                                                                                                                                                         259 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAS
                                                                                                                                                                       508 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteria;
                                                                                                                       DB
                                                                                                                       22;
                                                                        Indels
                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mechanism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cheese; yogurt;
                                                                                                                       1527;
                                                                        0;
                                                                        Gaps
                        651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6385
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527

TTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATT 586

Matches Query Match Best Local

l Similarity 87; Conser

Conservative

0; Score Pred.

Mismatches

Indels Length

0;

Gaps

0

No. 16;

DВ 84; 24;

8342;

3.2%;

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RESULT 28
ABL32500
ID ABL32500
ID ABL32500
AC ABL32
XX ABL32
XX ABL32
XX BUT 26-MA
XX Human
XX Gene;
XX Gene;
XX WO200
XX Homo
XX WO200
XX WO200
XX WO200
XX WO200
XX WO200
XX Homo
XX WO200
XX UCle
PH 01-SH
XX CENIC
XX Nucle
PT for c
XX Claim
XX C
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                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
      Sequence 8342
                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 473; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arterioscierosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                            diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL32500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAATGATACAAATACACCAATTAATCGTACTGCAGATGTTGATAAAATAGAAT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTAAAGAACCAAATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGGAGGAATTCGTCCCTCAGTTTCTTTGAAAACAATAACAGTTGAAGGACATGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAAAAAGAAAGATATTCAAAAGCCTAAAGTTGTTTTGAAACAAAATATCTATACTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTATTAACTATAAGAAATGACATTCACACTCCATATTTTTTAACTGAAGATTATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic; teriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                     methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000DE-1032529
2000DE-1043826
      BP;
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2037 A; 159 C; 2425 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated gene SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
   3721 T;
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   0
                                                                                                                                                                                                                                                                                                                                         German
   other;
                                                                                                                                                                                                                                                                                                                                                                                                                              abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful
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                                                                                             Matches
                                                                                                                     Query Match
                                       311654 TGTTGCGTATATGTTTGATAATACAGCTATTTTTGGTGTCGAAGGAAAAGACGCAGATGA 311713
                                                                                                                                                                                                                                    The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1842
                                                                                                                                                                                                 anti-Listeria vaccines.
Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                           antibodies and modulators
                                                                                                                                                                                                                                                                                                                                                                                      New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000; 2000FR-0012697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ67197;
                                                                                                                                               Sequence 1163020 BP;
                                                                                                                                                                                                                             treating infections by Listeria, and are useful as immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-332479/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2001; 2001WO-FR03061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200228891-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; Listeria; food contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria innocua contig DNA sequence #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ67197
               96
                                                                 36 TATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGA
                                                                                                         Local
ATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAATTTTTTATATTTGTTTTAGAATTTGGTTTTGGGATATGATTTTATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGTTTTTTTGATGATGTTACGTTAGGAAATTATTAAAATTTTTAAATTTTAGTTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                      printed specification, but was obtained in electronic format
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INST PASTEUR.
CNRS CENT NAT
                                                                                                                                                                       from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                              SEQ ID 10; 180pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glaser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                       3.1%;
                                                                                                                                              388339 A; 197589 C; 235612 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1163020
                                                                                           0,
                                                                                          Score 36.4; DB 24
Pred. No. 1.6e+02;
0; Mismatches 96
                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutational analysis;
                                                                                           Indels
                                                                                                                   Length
                                                                                                                                              341474 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                     for detection,
polypeptides,
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                                                                                                                     1163020;
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                                                                                         Gaps
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401978 GCTATTGGAACTTTTAATGGAAGCGGATATTGATGTTCGTGACATTTTAGACGAAGATGG 402037

ATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGT

155

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RESULT 30
ABQ69245
ID ABQ69
XX ABQ69
XX ABQ69
XX ANTID
XX Liste
XX ANTID
KW INfec
XX INST
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                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for the transfer of the sequences and are useful as immunogens in the sequences.
                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; SEQ ID 2058; 180pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
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                                                                      CC The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids counted to each probe of the microarray. The probes are useful for CC derived from mRNA of human breast, and then measuring the label CC centrying the expression of regions of genomic DNA predicted to centrying the expression of regions of genomic DNA predicted to centrying predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly considered the constraints.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spatially-addressable set of single exon nucleic acid probes, ful for measuring gene expression in sample derived from human
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30-JUN-2000;
03-AUG-2000;
                                                                                            measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention
                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human liver. The single exon nucleic acid probes may be used for precipitation.
                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dir
                                                                                                                                                                                                                                                           Claim
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SG,
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                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful
zing gene expression in human fetal liver -
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                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liver; gene expression; single exon nucleic acid
                                                                                                                                                                                                                                                        NO 14660;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
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                                                                                                                                                                                                                                                        sequence listing;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                            Single
hearts
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ABA33417
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derive from the human heart via microarrays. By measuring gene expression, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                  Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
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les 119; Conserv
                                                                                                                                                                                                                                                                                SG,
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2000US-0207456.
2000US-0608408.
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                                                                                                                                No 11883;
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                                                                                                                                                                                                                                                                                DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138;
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    gene expression, the
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RESULT 34
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ID AAK147
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XX O3-JUN
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Matches
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the prespecification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001
                                                                     WPI; 2001-483446/52
                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                               04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK14772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK14772 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
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                                                                                                                 Hanzel
                                                                                                                                                                                                          ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234687.
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; 2000GB-0024263.
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                                                                                                                 DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.18;
                                                                                                                 Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.2; DI
Pred. No. 5.7;
                                                                                                                 Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                         (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK40512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK40512 standard; DNA; 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 510
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                          2001-488900/53
                                                                            SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone marrow expressed exon;
                                                                                                                            MOLECULAR DYNAMICS
                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                     2000US-0180312.
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2000US-0608408.
2000US-0632366.
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                                                                                                                                                                              2000GB-0024263
                                                                                                                                                                                                        2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 A; 184 C; 68 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; lymphoma; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.2; DB 22;
Pred. No. 5.7;
0; Mismatches 138;
                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 36
AA14546/c
ID AA1455
AC AA1455
XX 17-OCT
XX Probe;
KW Probe;
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XX Hom
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Best Local :
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                                                                                                                                     03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #15232 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is one of the invention.
                                                                                            (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI46546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI46546 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 510 BP; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 15069; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 ATGCTGATGCAGGCGCTGATGCTGATGCAGGTATTGGTGTTGGTGCAGATGTTGATGCAG
                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTAGTGATGCTGGT
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119; Conserv
                                                                                            MOLECULAR DYNAMICS INC
                                              Hanzel DK,
                                                                                                                                     2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1%;
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                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5./;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36.2;
Pred. No. 5
                                                Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 G; 109
                                              DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic
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ABK7706
ABK77
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AC ABK77
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                     (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differential gene expression; genomic sequenced tag; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                   06-OCT-2000;
27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus clausii genomic sequence
Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second
                                                                              WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                            05-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus clausii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 ATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 CTGGTAGTGATGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTGCTGAAAAATGTGTTGATGCAAGTGCAGATGCTGATGCTGGTAGTGATGCTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTTGAAGCAGGTGCTGAAAAAGGTGTTGATGCAGGTGCAGATGCTGATGCTGGTAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCTGATGGTAGTGATGCTTGTGCAGATGTTGATGCAGATGTTGAAGCAGGTGTTGATG
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                                                                                                                                    ,70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; SEQ ID No 15232; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                     NOVOZYMES BIOTECH INC NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510
                                                                                                                                 Clausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                   2000US-0680598.
2001US-279526P.
                                                                                                                                                                                                                                                                                                                                            2001WO-US31437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                 iG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%;
46.3%;
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 5.7;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GST) #703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 510;
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CC isolated from Bacillus cells to a Substrate Containing array of Bacillus CC genomic sequenced tags (GST), examining the array, and determining CC relative gene expression by an observed hybridisation reporter signal of CC a spot in the array. The method is useful for measuring the expression of CC genes in a first Bacillus cell relative to expression of the same genes CC in one or more second Bacillus cells. The method is useful for monitoring CC global expression of several genes from a Bacillus cell, discovering new CC genes, identifying possible functions of unknown open reading frames and CC monitoring gene copy number variation and stability. Monitoring changes CC in expression of genes may be used to provide a representation of the way CC environmental stress or other physiological provocation. Extensive CC collow-up characterisation is unnecessary, when one spot on an array cequals one gene or one open reading frame, since sequence information is contained the contained t
                                                                                                                                               genes in a first Bacillus cell relative to expression of the genes other Bacillus cells, comprising hybridising labelled nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 5151; 200pp; English
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Query Match
Best Local
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                                                                                                                                  Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                Chemically pretreated genomic DNA associated with cell cycle #70.
                                                                                                                                                                                                                         18-DEC-2001
                                                                                                                                                                                                                                                AAS45434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTA 530
                                                                                                                                                                                                                                                                                                                                                                                    TCATCGCCGTATTTGCAATTTTGATCCTCTGGTCTTTTGCCGCCTGGTCATCCGCACCTG
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                                                                                                                                                                                                                        (first entry)
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56.2%;
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Pred. No. 8.
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뫄 δÃ 밁 Qy

Sequence 1103 BP;

232 A; 272 C; 270 G; 329 T; 0

other;

DВ

24;

Length 1103;

0

ftp.wipo.int/pub/published\_pct\_sequences.

밁 δÃ

15-MAR-2001; 2001WO-EP02945

20-SEP-2001

PCR primer.

sapiens

.mmunosuppressive;

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RESULT 39
ABK28281
ID ABK288
XX ABK28
XX ABK28
XX DNA t
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Best Local
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                                                                                                                                              DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; warardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HTV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK28281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with cell cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated genomic DNA #78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 7810
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59.0%;
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Pred. No. 20;
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Unidentified

Human colon cancer antigen encoding cDNA SEQ ID NO:1150

Human; colon cancer; colon cancer antigen; diagnosis; detection;

colorectal carcinoma;

SS.

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RESULT 40
AAH34068/c
ID AAH340
XX
AC AAH340
XX
AC AAH340
XX
DT 03-SEP
XX
DE Human
XX
KW Human;
KW colore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 sequences, and an oligomer, in particular an oligonucleotide CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical CC to the chemically pretreated DNA of genes associated with DNA CC transcription. The set of oligomer probes are useful for detecting the CC cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription CC diagnosing or treating diseases associated with DNA transcription CC (particularly with the methylation status), e.g. adenosine deaminase certain disorders, immunological disorders, Werner syndrome, CC thaematological disorders, immunological disorders, Werner syndrome, CC thaematological disorders, neurodegenerative disorders, Waardenburg CC syndrome, Niemann-pick disease, myelodysplastic syndrome, myocardial crifarction, hypertension, angiogenesis, erythropotesis, congenital heart CC disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription CC specification but was obtained in electronic format directly from the CC European Dataer of fetiar.
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                                                                                   03-SEP-2001
                                                                                                                                                     AAH34068
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7810 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000;
07-APR-2000;
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                                                                                                                                                                                                                                     TAGACGTTTGTGATGTATTTTATAGATTATTTGATAAAAGAATT
                                                                                                                                                                                                                                                                                                    TATGTTTAGTTTGATGTTTCGTGTATTTAATGTTTGGAGTGTTGTGGAATGTTTGTATTT 6609
                                                                                                                                                                                                                                                                                                                                     TTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACA 294
                                                                                                                                                                                                                                                                    ACAACTGTTGTCATTCGTTTCATCCATTATTTGTTACCAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-090046/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; SEQ ID No 155;
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIGENOMICS
                                                                                                                                                   standard; cDNA; 1481 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                 (first entry)
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1481 BP; 412 A; 259 C; 346 G; 459 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Sequence 5, Application US/09323427

Sequence 5, Application US/09323427

Patent No. 6248329

GENERAL INFORMATION:

APPLICANT: Chandrashekar, Ramaswamy

APPLICANT: Morales, Tony H.

TITLE OF INVENTION: Parasitic Helminth Cuticlin Profittle OF INVENTION: Molecules, and Uses Thereof

FILE REFERENCE: HW-8

CURRENT APPLICATION NUMBER: US/09/323,427

CURRENT FILING DATE: 1999-06-01

EARLIER APPLICATION NUMBER: 60/087,435
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Tony H.
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1161
TYPE: DNA
ORGANISM: Dirofilaria immitis
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US-09-812-642-5/c
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                                                                                                                            Sequence 5, Application US/09812642 Patent No. 6368600
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins,
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
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; TYPE: DNA
; ORGANISM: Dirofilaria
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Best Local Similarity
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Matches 1161; Conserv
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LENGTH: 1779
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                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/323, CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1779
TYPE: DNA
ORGANISM: Dirofilaria immitis
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GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Pro
TITLE OF INVENTION: Parasitic Helminth Cuticlin Pro
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
CURRENT FILING DATE: 1998-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER APPLICATION NUMBER: 05-01
EARLIER PETLING DATE: 1998-06-01
SEARLIER PETLING DATE: 1998-06-01
LENGTH: 1779
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GENERAL INFORMATION:

APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.

TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nuc
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1779
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US-09-812-642-1
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Best Local Similarity
Matches 1161; Conserv
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                                                                                                                                      FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/812,
CURRENT FILING DATE: 2001-03-20
                                                                                                                                                                     APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins,
TITLE OF INVENTION: Molecules, and Uses Thereof
                                                                                               PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Company
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER APPLICATION NUMBER: 60/087,435
UNUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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; ORGANISM: Dirofilaria
US-09-323-427-6
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US-09-323-427-7/c
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Best Local S
Matches 652
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic TITLE OF INVENTION: Molecules, and Uses Thereof TILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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Pred. No. 3.7e-137;
0; Mismatches 193;
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Patent No. 636600
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswam,
APPLICANT: Morales, Tony H.
                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 3
SEQ ID NO 6
LENGTH: 1372
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
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                                         TATTGACAATGGTGTCGAAGGTGAACCTGAAATAGAATGTGGCGCAGCTTCGATAACAAT 151
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; Sequence 7, Application US/09812642
; Patent No. 6368600
; GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nuc
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/99/812,642
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 09/323,427
; PRIOR APPLICATION NUMBER: 09/323,427
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
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TYPE: DNA
ORGANISM: Dirofilaria
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AAATCTGG
                                  GAGCCACATAGCGAATGTCCTCGACCACAATGCACAGAGCCACAAGGATTTGGTGCCATA
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RESULT 13 US-09-323-427-16

Sequence 16, Application US/09323427
Patent No. 6248329
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins,

Nucleic

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US-09-323-427-16
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Best Local S
Matches 554
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CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 892
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TYPE: DNA
ORGANISM: Brugia malayi
FEATURE:
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                                                      TCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCG
                                          TAATTTAATTAATGAAGAAGGATGTGCATTAGATCGATATCTTCTAAATAATTTGGAATA
                                                                                                   TGATACTTTCTGCGCGCGTTGTCCATTCCTGCTTTGTCGATGATGATGGTAACGGTGATACTGT
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Pred. No. 1.1e-124;
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TITLE OF INVENTION: Parasitic Helminth Cuticlin Pro-
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER FILING DATE: 1999-06-01
EARLIER FILING DATE: 1998-06-01
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 892
TYPE: DNA
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GENERAL INFORMATION:
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TCCAACTGATCTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCG
                                               TAATTTAATTAATGAAGAAGGATGTGCATTAGATCGATATCTTCTAAATAATTTGGAATA
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1.1e-124;
hes 155;
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RESULT 14 US-09-323-427-18/c ; Sequence 18, Application

US/09323427

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; NAME/KEY: CDS
; LOCATION: (158)..(892)
US-09-812-642-16
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16
LENGTH: 892
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Best Local Similarity
Matches 554; Conserv
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
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ORGANISM: Brugia malayi
FEATURE:
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Pred. No. 1.1e-124;
0; Mismatches 155;
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CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEO ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 892
TYPE: DNA
ORGANISM: Brugia malayi
US-09-812-642-18
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins,
TITLE OF INVENTION: Molecules, and Uses Thereof
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Pred. No. 1.1e-124;
0; Mismatches 155;
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; LOCATION: (1)..(813)
US-09-323-427-8
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US-09-323-427-8
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Best Local S
Matches 455
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CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 813
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 81
TYPE: DNA
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Pred. No. 7.7e-81;
0; Mismatches 161;
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CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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Patent No. 6248329
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Local Similarity 70.7%;
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                                                                                                                                   AATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGG-------
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SEQ ID NO 8
LENGTH: 813
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
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TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, TITLE OF INVENTION: Molecules, and Uses Thereof FILE REFERENCE: HW-8
CURRENT ELLING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US/09/812,642
CURRENT EILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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Best Local Similarity
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                                                                                                                                   GATTTGCTGCTGTAAAATCTGCTGCTGCACCAGCTCCAGAAGCTTCCTTGCTTTCTCCAC
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; LOCATION: (1)...(348)
US-09-308-003-45
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Best Local Similarity 53.2
"Chokes 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Burnham, Martin K. R.
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,
TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES
FILE REFERENCE: GM10093
NAME/KEY: CDS
LOCATION: (1)...(1179)
-09-308-003-8
                                                                                                                                        SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Appli
Patent No. 6326170
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/308,003
CURRENT FILING DATE: 1999-05-10
EARLIER APPLICATION NUMBER: 60/058,710
EARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES, TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES FILE REFERENCE: GM10093
                                                                                                                                                    NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                              APPLICANT: Burnham, Martin K. I
APPLICANT: Lonetto, Michael A.
APPLICANT: Warren, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/308,003 CURRENT FILING DATE: 1999-05-10
                                                                           TYPE: DNA
ORGANISM: Staphylococcus
                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Staphylococcus aureus FEATURE:
                                                                                                                  ENGTH:
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Pred. No. 0.6;
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US-08-894-017-24
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Patent No. 6024958
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                                       1426 GATGCTAAAGCTGATTACGAAGCAAAACTTGCTAAGTATCAAGCAGATCTTGCCAAATAT 1485
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-887-1500
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 31-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lehner, Thomas
APPLICANT: Kelly, Charles
TITLE OF INVENTION: POLYPEPTIDE FRAGMENTS CAPABLE
TITLE OF INVENTION: OF COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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925 CAAGCACGTCTTGCAAATGGT 945
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                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                            TOPOLOGY:
                                                                                                          Local
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                                                                                                                                                                                                                 LENGTH: 4865 base pairs
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90; Conserv
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                                                                                             Conservative
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Pred. No. 5.2;
0; Mismatches
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Pred. No. 1
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US-09-323-427-12/c
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LENGTH: 34
TYPE: DNA
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Query Match 2.9%; Sometime 2.9%; Sometime 100.0%; I Matches 34; Conservative 0;
                                                                                                                                                                      SEQ ID NO 12
LENGTH: 34
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Best Local
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                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/087,435
EARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic
TITLE OF INVENTION: Molecules, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/323,427 CURRENT FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Parasitic Helminth Cuticlin TITLE OF INVENTION: Molecules, and Uses Thereof
                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                           FILE REFERENCE: HW-8
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chandrashekar, APPLICANT: Morales, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: HW-8
                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                    OTHER INFORMATION:
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ilarity 100.0%;
Conservative
                                                                                     Description
Primer
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                 Score 34;
Pred. No.
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Pred. No.
                                                                                                   of Artificial Sequence:
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   Mismatches
                 DB 4;
0.47;
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US-09-812-642-12
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US-09-812-642-12/c
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Matches
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Patent No. 6368600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6368600
                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 11
                                                                                     Matches
                                                                                                                                                                                                                                                                        SEQ ID NO 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid TITLE OF INVENTION: Molecules, and Uses Thereof FILE REFERENCE: HW-8
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PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chandrashekar, APPLICANT: Morales, Tony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 18
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TYPE: DNA
                                                                                                                                                                                                                LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                       FEATURE:
                                                  696 GGCTGGCCAAGAAGCTCACGTATACAAATATGCG 729
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                   GGCTGGCCAAGAAGCTCACGTATACAAATATGCG
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ilarity 100.0%;
Conservative
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llarity 100.0%;
Conservative (
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Pred. No.
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                                                                                                                                                                             Artificial Sequence: Synthetic
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0.47;
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SEQ ID NO 91
LENGTH: 895
TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1445
LENGTH: 1521
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                                                                                                                                                     Matches
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.446C5
CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
CORRENADE: PRACTERO FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                           1005
                 945 GAAATGTATAGATGTATAACCAAATAATTTTCGTATAAAAGATTGATGTTCAAGTACACC
                                                                                                        623 AAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTTGGAATATC 682
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nes 67; Conserv
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Pred. No.
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Pred. No. 2
                                                                                                                                                 Mismatches
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RESULT 31
US-07-772-087-1
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US-09-134-001C-268
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APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
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LENGTH: 2427
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT:
                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1032
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                     APPLICATION NUMBER: UPFILING DATE: 19911008
                                      CLASSIFICATION:
                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
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les 75; Conserv
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5. 5275945
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Pred. No. 5.4;
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US-09-453-702B-166
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TELEX: 899149
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE H867 base pairs
                                                                                                                                                                                                                                                                                  Sequence 166, Applicat Patent No. 6365723 GENERAL INFORMATION:
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Best Local :
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STRAIN: 164A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Word Perfect 8.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    781 CCA 783
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LOCATION:
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OTHER INFORMATION: /product=
OTHER INFORMATION: 164A-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 96; Conserv
                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                 TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                   APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGTATATGGACGTATTGCA-TGTATCTCTCCCAGAAAAAGCAGCAGAAGCATTAAAAAA 972
                                                                                                                          CITY: Madison
                                                                                                                                      STREET:
                                                                                                                                      ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                               Application US/09453702B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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1022..1846
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716..1021
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                                                                                                                                                                                                                          Plunkett,
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                                                                                                                                                                                                                                         Nicole T.
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Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                       Valerie
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                                                1.44Mb storage
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FASULT 33
5.182210 -9/c
; Patent No. 5182210
; PATENT JOINT BINNS, MATTHEW M.; BOURSNELL, MICHAEL
; CAMPBELL, JOAN I.A.; TONLEY, FIONA M.
TITLE OF INVENTION: FOWLPOX VIRUS PROMOTERS
; NUMBER OF SEQUENCES: 22
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATAS.
; CURRENT APPLICATION DATAS.
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                                                                                                                                                                                                                                                                                       Query Match
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Best Local (
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  9055
                                                                                9112 ---TAGAAAAAGACTATTCTATGGAACAGGATATAGATAATAACGAAGATATCCGTACAG 9056
                                                                                                                                                                 9172 TAGAAACATCTTATTACAGTAAATTGAGTACTTATTTACTAACAAAAGCTGAAAGAGTAT 9113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1537 ATTATTCCTGAAATGTCCACTTGCTAC 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1477 TCAAATTGTTTGCTGATGTCCATAATATAACCCATTCCAATCTGCCATAAGTCCTCCTCA 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1417 GGTTGCTAAATCCTCCAACGCTTTTTCAACTTGCTGGGTTCAGATCATCAACGCCCCTGA 1476
                                       410 CTGAAATCACAACTGCTTTTCAAACTCAAATTG 442
                                                                                                                     350 ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT 409
                                                                                                                                                                                                        290 TAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCAT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 TGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCC 524
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                                                                                                                                                                                                                                               Local Similarity 55.0 nes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 11225
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 166:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
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ATGAAATGATAGCTGCTATAGAAGCTGAAATTG 9023
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TELEFAX: (608) 25
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/453,702B
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                                                                                                                                                                                                                                                                     55.68;
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                                                                                                                                                                                                                                               Score 33; DB 6; Length 11225;
Pred. No. 18;
0; Mismatches 65; Indels
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Pred. No. 17;
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RESULT 34

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RESULT 35
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NAME/KEY: misc_feature

; LOCATION: (1)...(630)

; OTHER INFORMATION: n = A,T,C

US-09-385-982-45
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                                                                                                                                                                                                                                                                             ;Patent No. 5352450
; APPLICANT: KOGA, TOSHIHIKO;OKAHASHI, NOBUO;TAKAHASHI, ICHIRO;SHIBUYA, KOJI;OHTA, HIROTAKA
; SHIBUYA, KOJI;OHTA, HIROTAKA
; CARIES AND VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-385-982-45
                                                                                                                                                                                                                                                                     DROP
                                                                                                                                                                             SEQ ID NO:
                                                                                                        Query Match
                                                                       Matches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: ENDEGE, WILSON O., ET AL
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Patent No. 62623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1998-08-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
1526 GATGCTAAAGCTGATTACGAAGCAAAACTTGCTAAGTATCAAGCAGATCTTGCCAAATAT 1585
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 630
                    274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      674 TGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGGATC 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 ATACTGTGGAAATTCTAAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   794 GTG 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    734 GATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCGAAT 793
                                                                     Local Similarity 48.0
                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                         LENGTH: 5177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAACCAGGAACAAGAATAGCTTATTGTTATCTGTGATAACACTGTTTTCTAAACACAAG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATACTGTTTCATATTTGAATCAGAGGGCTTCTTGTTCTGAGAAATAGGTTCAAAATCATT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                29-MAY-1990
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48.6%;
                                                                                    2.8%;
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                                                                                  Score 32.6;
Pred. No. 16;
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Pred. No. 5
                                                                     Mismatches
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                                                                                                      DB 6;
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                                                                   94;
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                                                                                                    Length 5177;
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FCT-US96-05320A-705
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PCT-US96-05320A-705/c
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                             Query Match
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                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Eric K. Steffe
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/470 FILING DATE: June 7, 1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/476,102
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 110
                                                                                                                                                                                                           NAME: Eric K. Steffe
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/487,429 FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3
COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS
               Local
                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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 l Similarity
60; Conserv
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                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVENTION:
                                                                                                                    576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application PC/TUS9605320A
                                                                                                                                                                    (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720 Rutland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America Johns Hopkins University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamilton O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9410 Key West Avenue
                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Genome Sciences
                                                                                                                                                                                 (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craig Venter
TION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome
                                                                                                                                                                                                                                                                                                                                                                               April22, 1996
                                                                                          double
                                                                                                                                                                 371-2540
               56.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
                                                                                                                                                                                                                                                                                                                                                                                              PCT/US96/05320A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20850
Score 32.4; DE Pred. No. 5.8; 0; Mismatches
                                                                                                                                                                                                              1488.014PC01
                            DB 5;
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                            Length 576;
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1038 TGCAGTACAAAATGGAATCTGCATGTCACCATTTGGCTTCTCAATGTTTATGGGTTTAAG 1097

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RESULT 37
US-08-781-802-5/c
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                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60
FILING DATE: 11-JAN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/019,580 FILING DATE: 12-JUN-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Reli
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION: 536
                                      FEATURE:
                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                        NAME/KEY: CDS
LOCATION: 197..1699
OTHER INFORMATION: OTHER INFORMATION: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     OTHER INFORMATION:
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 37
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/001,995 FILING DATE: 01-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                     NAME/KEY:
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                                                                                                                                                                                                                                       ENGTH:
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                                                                                                                                                                                                                                       4090 base pairs
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FONSTEIN, Michael
VONSTEIN, Veronika
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CASADABAN, Malcolm
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mat_peptide
197..1699
                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                              312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                           Mark
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                                                                                                                                                                                                   single
                                                 /note= "E011 sequence of longest
open reading frame; other possible start codons ATG/met4;
TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 60/009,704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-781-802-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
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                              REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 12-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VONSTEIN, Veronika
APPLICANT: DEMIRJIAN, David
APPLICANT: CASADABAN, Malcolm
                                                                                                                  FILING DATE: 07-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2655 AGAAGGAAACCCGCGGCTGTTTCGCGCCACAAATATTCTTGTTAATCAGA 2606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2775 ATATCCGATCGCCAAACCCCTTGTAAATAAAGGGGTTTCGGCATTTTATCTTTATATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2895 ACATGTTTTGAATAACGTCCATATGGTGAAGAAAATAGCAGCAGATTGATATCTCATTA 2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 TCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCT 269
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/694,078 FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
                                                                             NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       60606
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                 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FONSTEIN, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIKENS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALLEN,
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                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                      07-AUG-1995
                                                                                                                                                                                       10-JAN-1996
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                                                                                                                                                                                                         US 60/009,704
                                                                                                                                                    us 60/001,995
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                                                                  95,963-C
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Pred. No. 16;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 ACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                 ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch.

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                          PRIOR
                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Blattner, Frederick R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATCCGATCGCCAAACCCCTTGTAAATAAAGGGGGTTTCGGCATTTTATCTTTATATAGT 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTTCATCCATTATTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAGGAAACCCGCGGCTGTTTCGCGCCCACAAATATTCTTGTTAATCAGA 2606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129;
     APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                        CLASSIFICATION: <Unknown>
                                                                     APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                CITY: Madison
                                                                                                                                                                                                                                                                            ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                  OF SEQUENCES:
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197..1699
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open reading frame; other possible start codons ATG/met4;
TTG/leu7; GTG/val8; GTG/val15; GTG/val36; ATG/met62"
                                                                                                                                                                                                                                                                                                                                                                                                   Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                Guy
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Pred. No. 16;
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LENGTH: 1860
TYPE: DNA
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Best Local
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   964
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                                                                                                     148 GCAGGTATTGCTGTAGTTAATGATGATGGTACAAAACTTTTTAAAGAAAAAGGAAGAATT
                                                                                                                                     844 GGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCT 903
                                                                                                                                                                                                     784 AATAGCGAATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGGAGCTGTTAAAACA 843
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GATAATCAAGCTTTGCCAGTTGATTTACGTCACCGTGCACTTCTGCAACATAATGGACAA 1023
                                 GCTGAATTACGTAAAGTTGCAGATAATAGTGATGAGGATGGTACGTTAGGAATTGGTCAT
                                                                 GCAGAACCGGAGAATATCATTGATGTACGAACTGATATCAACACCCTTGAAAATTAGCGAT 963
                                                                                                                                                                   AATGCCAAAGAATTACTATTAAAAGGGTTAGAAAAATTAGAATATCGTGGTTATGACTCA 147
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Conservative

2.8%;

Score 32.2; Pred. No. 1

DB 4;

Length 1860;

Mismatches

148;

Indels

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Gaps

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RESULT 40
US-09-134-001C-1411
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                                                                                                                    Sequence 1411, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
EILE REFERENCE: GTC-007
                                        CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      931 ATGAGCACTATTACACTTAAAAAAGCAGAAGCAAATATAAAAGAGAAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTTGACAATGGTGTCGAAGGTGAGCCAGAA---ATTGAATGTGGACCAACTTCAATAACA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             ATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTATTMTACTGCTGACATTCTCATGTACAAAAGGTCTGGCATTTGACATTTCCATGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 31960
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268 ACACGITGGGCGACACATGGIGTTCCAAATTATGAAAATTCACATCCACACCAGTCAACA 327
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Search completed: March 28, 2003, 17:00:55 Job time: 141 secs

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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1161
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//cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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//cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
//cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
//cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
//cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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                     US-10-054-562A-3
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8233.163 Million cell updates/sec
Sequence 3, Appli
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Sequence 2, Appli
Sequence 6, Appli
Sequence 16, Appli
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Sequence 10, Appli
Sequence 3231, Appli
Sequence 1883, Ap
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Sequence 31, Appli
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RESULT US-10- ; Sequ ; Pate ; GENE ; APP			) (					C					G			C											
ULT 1 10-054-562 equence 3, atent No. 1 ENERAL INF APPLICANT: APPLICANT:		51	4	4.2	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
RESULT 1  US-10-054-562A-3  ; Sequence 3, Application US/10054562A ; Patent NO. US20020165375A1 ; GENERAL INFORMATION: ; APPLICANT: Chandrashekar, Ramaswamy APPLICANT: Morales, Tony H. ; TITLE OF INVENTION: PARASITIC HELMI		33.4	ب د د د	22. 6	33.8	33.8	33.8	34	34	34	34	34	34	34	4	34.2	34.6	34.6	34.8	34.8	34.8	34.8	34.8	34.8	35	35	
2A-3  J. Applicat J. Sapplicat US2002016  FORMATION: C. Chandras C. Morales C. WELLINGTON: C. WELLINGTON:		2.9		) k	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9	3.0	3.0	з. О	3.0	3.0	з. О	3.0	3.0	3.O	3.0	
2A-3 , Application US/100: US20020165375A1 FORMATION: Chandrashekar, Rame Morales, Tony H. INVENTION: PARASITIC		16950	200	4239	32768	1182	1170	6035	2322	895	556	325	34	34	3549	402	21252	1479	8395	6617	1959	1611	1608	583	962	660	
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10054562A Ramaswamy H. H. H.CTIC HELMINTH CUTICLIN PROTEINS,	ALIGNMENTS	US-10-114-170-166	IIS-09-070-927A-302	US-09-938-842A-4475 US-08-781-986A-333	US-09-070-927A-100	US-09-815-242-8204	US-09-815-242-4340	US-08-781-986A-272	US-09-764-872-725	US-09-745-288-91	US-09-864-761-8619	US-09-864-761-25339	US-10-054-562A-12	US-10-054-562A-11	US-09-070-927A-859	US-09-960-352-11958	US-09-070-927A-94	US-09-070-927A-405	US-09-070-927A-217	US-10-210-296-1	US-09-864-761-4012	US-09-815-242-6630	US-09-815-242-3929	US-09-864-761-20772	-09-864-761	US-09-864-761-19488	
, NUCLEIC ACID MOLECULES,		Sequence 166, App	Seguence 302 App	Sequence 44/5, Ap	Sequence 100, App	Sequence 8204, Ap	Sequence 4340, Ap	Sequence 272, App	Sequence 725, App	Sequence 91, Appl	Sequence 8619, Ap	Sequence 25339, A	Sequence 12, Appl	Sequence 11, Appl		Sequence 11958, A	Sequence 94, Appl	Sequence 405, App	Sequence 217, App	Sequence 1, Appli	4012,			20772	Sequence 2772, Ap	Sequence 19488, A	

## ; NAME/KEY: CDS ; LOCATION: (1)..(1161) ; OTHER INFORMATION: US-10-054-562A-3 TITLE OF INVENTION: THEREOF FILE REFERENCE: HW-8-2 CURRENT APPLICATION NUMBER: US/10/054,562A CURRENT FILING DATE: 2002-06-10 PRIOR APPLICATION NUMBER: 09/812,642 PRIOR FILING DATE: 2001-03-20 PRIOR FILING DATE: 1999-06-01 PRIOR FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 18 밁 Qy 망 QΥ SOFTWARE: Query Match Best Local Similarity Matches 1161; Conserv LENGTH: 1161 TYPE: DNA ORGANISM: Dirofilaria immitis FEATURE: 121 AATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAA 61 PatentIn Conservative version 3.1 100.0%; Score 1161; DB 9; 100.0%; Pred. No. 4.7e-294; tive 0; Mismatches 0; Length 1161; 0; Gaps 180 60 60 0;

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TTTCGTCCAAATCAGAAGGCA
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RESULT 2 US-10-054-562A-5/c

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GENERAL INFORMATION:

APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.

APPLICANT: Morales, Tony H.

TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
CURRENT APPLICATION NUMBER: US/10/054,562A .

CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 1199-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5
LENGTH: 1161
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Best Local Similarity 100.0%;
Matches 1161; Conservative 0;
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Pred. No. 4.7e-294;
Mismatches 0;
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1779
TYPE: DNA
ORGANISM: Dirofilaria immitis
US-10-054-562A-1
                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chandrashekar, Tony H.
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PARASITIC HELMINTH CUTICI,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 109/812,642
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PRIOR APPLICATION NUMBER: 09/812,642
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Best Local Similarity 100.0%;
Matches 1161; Conservative 0
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                                                                                                       Score 1161; DB 9;
Pred. No. 6e-294;
Mismatches 0;
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APPLICANT: Chardishekar, Ramaswamy
APPLICANT: Chardishekar, Ramaswamy
APPLICANT: Chardishekar, Ramaswamy
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2001-03-20
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PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1779
TYPE: DNA
ORGANISM: Dirofilaria immitis
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Matches 1161; Conserv
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                                                                                                              GGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCCAGTTTATCATAAATGG
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  AATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAA 180
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CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEO ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                 ; TYPE: DNA; ORGANISM: Dirofilaria immitis US-10-054-562A-6
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US-10-054-562A-6
                                                                                                                                Query Match
Best Local S
Matches 652
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: HW-8-2
                                                                                                                                                                                                                                               LENGTH:
ATGATGATTCGTCTTATTGCTTTCTGTACTACACTTATTG-CATTGTCTTATTCGATTCC 59
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Pred. No. 5.1e-122;
0; Mismatches 193;
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                US-10-054-562A-7
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GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PRASITIC HELMINTH TITLE OF INVENTION: THEREOF
                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 7
                                                                                    FILE REFERENCE: HW-8-2
CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
                       LENGTH: 1372
TYPE: DNA
ORGANISM: Dirofilaria
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RESULT 7
US-10-054-552A-16
; Sequence 16, Application US/10054
; Patent No. US20020165375A1
; GENERAL INFORMATION:
; APPLICANT: Chandrashekar, Ramasw
; APPLICANT: Morales, Tony H.
; TITLE OF INVENTION: PARASITIC HE
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; TYPE: DNA
; ORGANISM: Brugia malayi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (158)..(892)
; OTHER INFORMATION:
US-10-054-562A-16
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 892
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Best Local Similarity
Matches 554; Conserv
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                                              TAATTTAATTAATGAAGAAGGATGTGCATTAGATCGATATCTTCTAAATAATTTGGAATA
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Pred. No. 8.2e-111;
0; Mismatches 155;
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PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOETWARR: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 892
TYPE: DNA
ORGANISM: Brugia malayi
US-10-054-562a-18
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US-10-054-562A-18/c
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Patent NO. US20020165375A1
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REFERENCE: HW-8-2
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Best Local 9
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
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                                                                   TAATTTAATTAATGAAGAAGGATGTGCATTAGATCGATATCTTCTAAATAATTTGGAATA
                                    GGAAATTCTAAATGCTGATGATGTGCTCTTGATAAATATTTTGCTAAATAATTTTGGAATA
                                                                                                                                                                       TGTCCCGATGCCAGTATGCCGTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGT
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Pred. No. 8.2e-111;
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CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEO ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEO ID NO 8
LENGTH: 813
TYPE: DNA
ORGANISM: Dirofilaria immitis
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; LOCATION: (1)..(813)
; OTHER INFORMATION:
US-10-054-562A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 455; Conserv
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
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GTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA 943
                                                                                                                             AATGTGTTCGACCACAATGTTCAGAACCACAAGGATTCGG-------
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                               GATTTGCTGCTGTAAAATCTGCTGCTGCACCAGCTCCAGAAGCTTCCTTGCTTTCTCCAC
                                                             -----AGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTC 883
                                                                                              AATGTCCTCGACCACAATGCACAGAGCCACAAGGATTTGGTGCCATAAAATCTGGACAAG
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70.7%;
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GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
FITTLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PRO-
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR APPLICATION NUMBER: 09/813,427
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEO ID NOS: 18
SOFTWARE: PatentIn version 3.1
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Patent No. US20020165375A1
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Best Local
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884 GTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTGATATCA 943
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                               320 GATTTGCTGCTGTAAAATCTGCTGCTGCACCAGCTCCAGAAGCTTCCTTGCTTTCTCCAC
                                                                                                                                                                            ATCGATCACAGCTTTTCTATCAATGCCAGATCAGTATTACCATTAAAGAACCAAATAGCG 790
                                                                                                                                                                                                                        ATTTGGAATATCCAACAGATTTAATGGCTGGCCAAGAAGCTCACGTATACAAATATGCGG
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                                                                                            AATGTCCTCGACCACAATGCACAGAGCCACAAGGATTTGGTGCCATAAAATCTGGACAAG
                                                                                                                                                         ATCGATCAGAACTTTACTATCAATGCCAGATTAGTATAACAATTAAAGAGCCACATAGCG
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APPLICANT: KIEPS, JOEL
APPLICANT: KIEPS, JOEL
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/257,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/300,111
                                                                                              RESULT 12

US-09-902-941-1883/c

; Sequence 1883, Application US/09902941

; Patent No. US20020172952A1

; GENERAL INFORMATION:
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US-09-938-842A-3231
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Best Local Similarity
Matches 147; Conserv
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    APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watnabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harper, Jeff
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Pred. No. 2;
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RESULT 14
US-10-017-754-1883/c
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Best Local
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RESULT 13
US-09-849-626-1883/c
US-09-849-626-1883/c
; Sequence 1883, Application US/09849626
; Sequence 1800, US20020197669A1
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APPLICANT: Fanger, Gary R.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
NUMBER OF SEQ ID NOS: 2002
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-1883
                                                                                                                                                                                                                                                                                           SEQ ID NO 1883
LENGTH: 6799
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.3%;
Best Local Similarity 59.1%;
Matches 65; Conservative
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APPLICANT: Switzer, Anne
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
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                                                                                                                  235 TTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACA 294
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GTACCTGTGCTGACTTTATTTCCTAGATGATTTATTCCTTTATTTTATGG
                                          ACAACTGTTGTCATTCGTTTCATCCATTATTTGTTACCAAAGTTGATCG
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Wang, Tongtong
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                     3.3%;
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Pred. No.
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Pred. No. 15;
0; Mismatches
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; ORGANISM: Homo sapiens
US-10-017-754-1883
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                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
                          PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-x-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 ACAACTGTTGTCATTTCATCCATTATTTGTTACCAAAGTTGATCG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.3%;
Local Similarity 59.1%;
les 65; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel, David K.
Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter, Darrick
Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marnerakis, Margarita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vedvick, Thomas S.
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       PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB (
Pred. No. 15;
0; Mismatches
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15;
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GENERAL INFORMATION:

APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth

TITLE OF INVENTION: Methods For Monitoring Multiple

TITLE OF INVENTION: Expression

FILE REFERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/680,598
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Sequence 5151, Application US/09974300 Patent No. US20020146721A1

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OTHER INFORMATION: E
RESULT 16
US-09-974-300-5151
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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SOFTWARE: Annomax Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00662 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                        536
                                                                                                                                                                                                                                                                                                                                                                                                                     476 ATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTTGGTCAGCCAGTTTATCATA 535
                                                                                                                  716 TATACAAATATGCGGAT 732
                                                                                                                                                                                               596
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                                                                                                                                                                                                                                                                                                                                                                                          414 ATGCTGATGCAGGCGCTGATGCTGATGCAGGTATTGGTGTTGGTGCAGATGTTGATGCAG 355
                                                                              174 CTGGTAGTGATGCTGGT
                                                                                                                                                                                                                                     294 ATGCTGATGGTAGTGATGCTTGTGCAGATGTTGATGCAGATGTTGAAGCAGGTGTTGATG 235
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FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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                                                                                                                                                           CAGGTGCTGAAAAATGTGTTGATGCAAGTGCAGATGCTGATGCTGGTAGTGATGCTGATG
                                                                                                                                                                                                                                                                           ATGTTGAAGCAGGTGCTGAAAAAGGTGTTGATGCAGGTGCAGATGCTGATGCTGGTAGTG
                                                                                                                                                                                                                                                                                                                                                    AATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTGTCCATTCCTGCTTTG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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EXPRESSED IN HEART, SIGNAL = 0.85
EXPRESSED IN BRAIN, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL = 0.9
EXPRESSED IN BY474, SIGNAL = 4.6
EXPRESSED IN FYATAL LIVER, SIGNAL = 0.93
EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
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                                                                              158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138;
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 5151
LENGTH: 1103
TYPE: DNA
ORGANISM: Bacillus clausii
                                                                    US-08-781-986A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 17
US-08-781-986A-33
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        Matches
                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                           TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 7563 base pairs
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charles TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          812
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                                                                               TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 C 591
                 Local
                                                                                                                                                                                                                                     NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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les 68; Conserv
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    . Similarity 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Human Genome Sciences,
9410 Key West Avenue
    Conservative
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              3.0%;
53.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                 version 6.2
                                                                                                                                                                                                                           PB248PP
 Score 35.4; r
Pred. No. 79;
0; Mismatches
    0;
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Pred. No. 16;
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                                DB 7;
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                                Length 7563;
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0;
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Gaps
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY M.
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                       Sequence 1160, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09901136 Publication No. US20030039968A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279686 ATGCAGGTCTCAGTATTGCTGGAATAAGAAAGAAAATCACCTGTTTTAAACATAAGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HU, Song et al.

APPLICANT: HU, Song et al.

TITLE OF INVENTION: INCLEDIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CL001273
                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(378361)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCATGCAATGTTGCGCGTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGCATTCGAAGGACATGTT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGGTATGCCTGAAGGAGAATATGATTTGGGTGGACAAAAAGTAACTGTTCAATCGCAA 5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGCTTACCGTATGAAAGGTAATGAACGTTTTTATTTAATTACCGATGCAATGCGTGCA 5535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTC
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Pred. No. 6.2e+02;
0; Mismatches 66
                                                                                                                                               BY MICROARRAY
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APPLICATION NUMBER:

2000-10-04 2000-08-

US 60/236,359

GB

24263.6

APPLICATION NUMBER:

NUMBER: US 09/632,366

FILING DATE:

2000-09-

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RESULT 20
US-09-864-761-19488
; Sequence 19488, Application US/09864761
; Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 58; Conserv
                               APPLICANT: Penn, Sh
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                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER
OTHER
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TYPE: DNA
ORGANISM: Homo sapiens
   APPLICANT:
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                                                                                                                                                                                                                                          CGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTTCAATAACAA 118
                                                                                                                                                           GCAATTCCACTACTGGGTATATATCCAAAGGAAATG
                                                                                                                                                                                                                        CCGTGGAAAACAGTATGGAAGTTCCTCAAAAAATTAAAACTAGAACTACCGTATGAACCA 236
                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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Penn, Sharron G.
Rank, David R.
Hanzel, David K.
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EXPRESSED IN BONE
EXPRESSED IN HBL1
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D IN BT474, SIGNAL = 1.7
D IN FETAL LIVER, SIGNAL = 3
D IN LUNG, SIGNAL = 1.6
D IN HELA, SIGNAL = 3.1
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                                                                                                                                                                                                                                                                                   Score 35.2; D: Pred. No. 18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADULT LIVER, SIGNAL - BRAIN, SIGNAL - 3.6
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HBL100, SIGNAL = 5.2
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Best Local
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NUMBER OF SEQ ID NOS: 49117
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/608,408
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AGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
                                                                                    GTGATGATGATGGATATGGTGGTGATGATGCTGATGGTGATGATGGTTATGGTGGTG 180
                                                                                                                           GTTATGAAATTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTC 520
                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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2000-06-30
US 09/774,203
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EXPRESSED IN BT474,
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NT HIT: AF
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                                                                                                                                                                                                                                                                                                                                              ED IN HBL100,
AF044255.1, F
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                                                                                                                                                                                                0;
                                                                                                                                                                                             Score 35; DB Pred. No. 25; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                              N PLACENTA, SIGNAL = 5

N HEART, SIGNAL = 1.1

N HELLA, SIGNAL = 3.8

N HELLO, SIGNAL = 3

44255.1, EVALUE 1.10e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N BONE MARROW, SIGNAL = 6

N LJUNG, SIGNAL = 2.9

N BRAIN, SIGNAL = 6.5

N ADULT LIVER, SIGNAL = 5

N RETAL LIVER, SIGNAL = 1
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PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PRILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04

PRIOR PRILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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                                                                      SOFTWARE: Annomax
SEQ ID NO 2772
LENGTH: 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
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                                                                                                                                               APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                        APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
       INFORMATION:
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Hanzel, David K.
     MAP
   TO AC008125
                                                                                                               Listing Engine vers. 1.1
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Best Local :
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                                                                        PRIOR
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 DATE
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NUMBER: PCT
: 2001-01-30
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521 AGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTTG
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                                                                                                 TCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGATG
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                                       GATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCTG
                                                                            ATGGTTATGGTGGTGATGATGGTTATGGTGGTAATGATGCTGATAGTAATGATGATG
GTTATGGCAGTGACGATGCTGATGGTAATGATGGTTATGGCAGTGACGATGCTGATG
                                                                                                                                                         ATGATGCTGATGGTGATGGTGGTGATAGTGATGGTGAGGATGCTGATCGTGATGATG
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IN LUNG, SIGNAL = 2.9
IN BRAIN, SIGNAL = 2.9
IN ADULT LIVER, SIGNAL = 5
IN FETAL LIVER, SIGNAL = 1
IN PLACENTA, SIGNAL = 1.1
IN HEART, SIGNAL = 3.8
IN HELA, SIGNAL = 3.8
IN HELA, SIGNAL = 3.8
IN HELA, SIGNAL = 3.8
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US-09-864-761-20772; Sequence 20772, Application US/09864761 APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1

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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30 ACID PROBES USEFUL

PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30

FILING DATE:

APPLICATION NUMBER: PCT/US01/00663

2001-01-30

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; OTHER INFORMATION: US-09-864-761-20772
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US-09-815-242-3929
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PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                             APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
                                                                                                                                                                                                                                  GENERAL INFORMATION:
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SEQ ID NO 20772
LENGTH: 583
                                                                                                                                                                                                                                                  Sequence 3929, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
              TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/09/815,242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                    Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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N: EXPRESSED IN BT474, SIGNAL = 1.9

N: EXPRESSED IN BRAIN, SIGNAL = 2.1

N: EXPRESSED IN LUNG, SIGNAL = 1.7

N: EXPRESSED IN HBL100, SIGNAL = 2.3

N: EXPRESSED IN HELA, SIGNAL = 2.7

N: EXPRESSED IN PACCENTA, SIGNAL = 2.2

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
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AW992395.1, EVALUE 9.50e-02
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; ORGANISM: Enterococcus
US-09-815-242-3929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                 PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                               PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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o. US20020061569A1
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Yamamoto, Robert T.
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                  Xu, H. Howard
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Pred. No. 47;
0; Mismatches
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US-09-864-761-4012

; Sequence 4012, Application US/09864761

; Patent No. US20020048763A1
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; LOCATION: (1)...
US-09-815-242-6630
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PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00664
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR PPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: AGOMICA-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/832,366
PRIOR APPLICATION NUMBER: US 09/832,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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SEQ ID NO 6630
LENGTH: 1611
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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ORGANISM: Enterococcus
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                                                                                    APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
                                                                 APPLICATION NUMBER: PCT/US01/00670
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E: 2001-01-30
N NUMBER: US (
E: 2000-09-21
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Pred. No. 47;
0; Mismatches
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-4012
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                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 1
    Matches
                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10210296
Publication No. US20030021802A1
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                                                                                                                                                                                                                                                                APPLICANT: Pfizer Products Inc.
TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS,
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: AND MATERIALS
TILE REFERENCE: PC10589A
CURRENT APPLICATION NUMBER: US/10/210,296
CURRENT FILING DATE: 2002-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                         CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/689,065
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                   TYPE: DNA ORGANISM: Lawsonia intracellularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO ALO22334.1

OTHER INFORMATION: EXPRESSED IN BTA174, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HBLL100, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HBLA.05, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HBLA.05, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.7
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                                                                                                                                           LENGTH: 6617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGATGGTGATGATGACATTAGAAAGA 966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
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3.0%;
ilarity 50.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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    0;
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Pred. No. 52;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                       Score 34.8;
Pred. No. 1
    Mismatches
                   8; DB 9;
1e+02;
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    82;
                                      Length
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1959;
                                                                                                                                                                                                                                                                                                                                                                        AND RELATED
  0;
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  Gaps
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AGAAATTGAATGTGGACCAACTTCAATAACAATCAATTTTAATACACGTAATGCATTCGA 146

밁 Š 밁 Qy В

CITY: Rockville STATE: Maryland

STREET: ADDRESSEE:

COUNTRY:

20850

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US-09-070-927A-217/c
: Sequence 217, Application US/09070927A
: Patent No. US20020120116A1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 217:
                                                                                                            4247 GATGCCTATATTTCTGTTGTAGAAGCATTAAAACATGCTGGGTTTGATTTTGATTCAGAT 4188
                    4187 ATCGAAATTGATTGGGTTGATTCACAAGAATTAACTGCTGAAAATGTCGCTGAAAGAATT 4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1610 TCTTCGTGCATTAGAATATGGAATGCCACCAGCAGCAGGGGAAGGT 1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1490 AGAAATTGCTAATGCATTTTCAGAACTTAATGATCCTATTGATCAACGTCTGCGTTTTGA
                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 8395 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 217:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAACAAGTTCTTGAGAAAGCACGTGGAGAAGAAGCATGTCCCCATGGATGAAGATTA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9410 Key West Avenue
                                                                                                                                                                                                                       3.0%;
53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309-8512
                                                                                                                                                                                                       0;
                                                                                                                                                                                                     Score 34.8; DB 10
Pred. No. 1.2e+02;
0; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PB369
                                                                                                                                                                                                                                              DB 10;
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                                                                                                                                                                                                                                            Length 8395;
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Sequence 405, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 405:
                                                                                                                                                                                1121
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                                                                                                                                                                                                                                                                   1061 AAGAACAATTATTATAATGAATTTAGCGAATATGAAAATGACATCATGCAAGGAATTGT 1120
                                                                                                                                                                                                                         171
                                         291 AACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCATA 350
                                                                                                                                                                                                                                                                                          111 AATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,3
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                       TTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTTCAGCAGATGG 4114
ATCACGTGTTGAAAACAATTCAAAAAGGCCCACAAGTTTTTGTAAGCCGTAGTCATCCAGA 1300
                                                                                     AAAACAAGATCAAATGCCAAATGAATTTTACCAACCGCATGRTCGGRTTAAAGTTTACGT 1240
                                                                                                                                 TCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGT 290
                                                                                                                                                                             TGAACGTCAAGATCGTCGTTATATTTATGTAAACTTAGGTAAAATCGAAGCAGTCTTATC 1180
                                                                                                                                                                                                                                                                                                                                                           136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1479 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Scie
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (301) 309-8504
301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                              3.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                              Score 34.6;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40,302
                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                           170;
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721 AAATATGCGGATCG 734

US-09-070-927A-217

STRANDEDNESS:

TELEFAX: (301)

Matches

Local Similarity es 72; Conserv

Conservative

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US-09-070-927A-94/c
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                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 21222 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 94, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                            1641 AAAAAGCCAGTTGAAGAATCTGTTCACACATCAACTGAAACAACAGTGAAATCATCCACT 1582
                                                                                                                                                                1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1361 CGTAAGC 1367
                                                                                                                                                                                                  283 ATTTTTGTAACAACACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGAT 342
                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kebley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 982 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                          ATTGCTGGGATTTTATCTGTGATTATTATGTTTGGTGCGGTAATTTTTGTCTTTTTTGGC 1642
                                      GAGGTATCTGAAATCACAACTGCTTTTCAAACT 435
                                                                                                                  CGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAATC 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTACTAAAACGKCTTTTTGAACAAGAAATTCCAGAAGTTTATGATGGAATTGTTGAAAT 1360
                                                                                                                                                                                                                                            l Similarity
79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9410 Key West Avenue
                                                                                                                                                                                                                                                               3.0%;
                                                                                                                                                                                                                                            Score 34.6; DB 10
Pred. No. 2.3e+02;
0; Mismatches 74
1549
                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  storage
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                  Length 21252;
                                                                                                                                                                                                                                          0;
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RESULT 31
US-09-070-927A-859/c
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; OTHER INFORMATION: Clone ID: 51-LIB34-002-Q1-E1-E4
US-09-960-352-11958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 30
US-09-960-352-11958/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 859, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11958, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION TITLE OF INVENTION. MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nagappan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 920 TCATTGATGTACGAACTGATATCAACACCCT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860 AACCTGCTGCAGCTGCGCAACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOPTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Ger
                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCATCTCTTCCAACAAAGGCTCCTCGGCCTCGGAACAAATCTGCAGAAATGGGCCAAAA 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                   APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                       APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steven Barash
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Pred. No. 30;
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                                                                                                                                                                                                                                                       3.50 inch, 1.4Mb storage
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US-10-054-562A-12/c

; Sequence 12, Application US/10054562A

; Patent No. US20020165375A1
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                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Primer US-10-054-562A-11
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Best Local Similarity
Matches 75; Conserv
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Best Local Similarity
                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10054562A Patent No. US20020165375A1
                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/054,562A CURRENT FILING DATE: 2002-06-10 PRIOR APPLICATION NUMBER: 09/812,642 PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: MOZALES, TONY H.
TITLE OF INVENTION: PARASTIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                    LENGTH: 34
TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                        696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                     GGCTGGCCAAGAAGCTCACGTATACAAATATGCG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTTGTTGAAGGCTTTTTTCTGCCGTTGCAGTTTGTCGTACTTTTTCTTCATAATTTGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGA 404
                                                                                                                                                                         34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-11-14
                                                                                                                                                                      2.9%;
ilarity 100.0%;
Conservative
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Pred. No
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Pred. No. 1.1e+02;
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8.4;
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APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25339, Applicatio Patent No. US20020048763A1
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SEQ ID NO 12
LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              696 GGCTGGCCAAGAAGCTCACGTATACAAATATGCG 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
                                      FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT,
                                                                                 APPLICATION NUMBER: PCT/US01/00663
                                                                                                      APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/236,359
                                                                                                                                                   FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-10-04
                  FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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Rank, David R.
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NUMBER: PCT/US01/00661
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                                        PCT/US01/00662
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Pred. No.
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PRIOR FILLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-08-03
PRIOR PPLICATION NUMBER: US 09/632,366
PRIOR PPLICATION NUMBER: GB 4263.6
PRIOR PRILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILLING DATE: 2000-09-27
PRIOR PILLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8619, Application Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25339
LENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                               APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
                                                                                     APPLICATION NUMBER: PCT/US01/00669
                                          APPLICATION NUMBER: PCT/US01/00665
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                       2001-01-30
                                                                  2001-01-30
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EXPRESSED IN PLACENTA, SIGNAL = 1.6

EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

EXPRESSED IN HEART, SIGNAL = 1.8

EXPRESSED IN FETAL LIVER, SIGNAL = 2.2

EXPRESSED IN FETAL, SIGNAL = 1.9

EXPRESSED IN HELA, SIGNAL = 1.9

NT HIT: AF164151.1, EVALUE 6.80e-01

EST_HUMAN HIT: BE336733.1, EVALUE 3.20e+00
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PCT/US01/00668
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OTHER INFORMATION: EXPRESSED IN PLACE
OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN HEART
OTHER INFORMATION: EXPRESSED IN FETAL
OTHER INFORMATION: EXPRESSED IN HELA;
OTHER INFORMATION: EXPRESSED IN HELA;
OTHER INFORMATION: EXPRESSED IN HELA;
                                                                                                                                                                                            US-09-745-288-91
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 91
LENGTH: 895
                                                                                                                                    Best
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                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.446D1
CURRENT APPLICATION NUMBER: US/09/745,288
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 91, Application UPatent No. US20010018058A1
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LENGTH: 556
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                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
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ORGANISM: Homo sapiens
342 TCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGAT 401
                                          150
                                                            282 TATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGA 341
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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ETLING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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                                     TATATCCTTAACTTCAATTATTGTCACTTATAAATAAAGGTGATTTGCTAACACATGCAT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
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                                                                                                                 67;
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                                                                                                                 Conservative
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                                                                                                                                Score 34;
Pred. No.
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Pred. No.
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N HEART, SIGNAL = 1.8

N HEART, SIGNAL = 1.8

N FETAL LIVER, SIGNAL = 2.8

N HELA, SIGNAL = 1.9
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                                                                                                                              DB 54;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-725
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US-08-781-986A-272/c
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US-09-764-872-725/c
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 272, Application US/08781986A Publication No. US20030054436A1 GENERAL INFORMATION:
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Best Local Similarity 54.9%;
Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/764,872 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 957
                                                                                                                  COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2059 TG 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2119 TTGTGAACACAGATGCCAAAAATTATACATGTAAGTTAATGCACAACAAGAGTATACAC 2060
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 TCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGAT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 TG 403
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                 APPLICATION NUMBER: FILING DATE:
                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                    STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                    STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                     Diskette,
                                                                                                                                                                                                                                                                                                      Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus Polynucleotides : 5255
                                                                                                   US/08/781,986A
                                                                                                                                                                                   3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 94;
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; ORGANISM: Staphylococcus aureus US-09-815-242-4340
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                                                                                                                                                     SEQ ID NO 4340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.9%;
Best Local Similarity 50.6%;
Matches 82; Conservative
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/2
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 14110
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                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5838 TGGCCGCTTTGACATATACGGACCTCAAATATTAATTCAAGA 5797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 TGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTTGTAACAAC 296
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu, H. Howard
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Score 33.8; D
Pred. No. 71;
0; Mismatches
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Pred. No. 1.6e+02;
0; Mismatches 80
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                                       DB 10;
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                                       Length 1170;
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Matches

Conservative

0;

Gaps

0;

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16

796 ATTGCTTACCGTATGAAAGGTAATGAACGTTTTTATTTAATTACCGATGCAATGCGTGCA 855

ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTTGACAATGGTGTC 75

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APPLICANT: Xu, H. HOWARD

TITLE OF INVENTION: Identification of Essential Genes in ITILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-10-2-16
NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1182)
US-09-815-242-8204
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                                                                                                                                                                                                                                                        Query Match 2.9%;
Best Local Similarity 52.5%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8204
LENGTH: 1182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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tent No. US20020061569A1
925 CAAGCACGTCTTGCAAATGGT 945
                                                                             865 AAAGGTATGCCTGAAGGAGAATATGATTTGGGTGGTCAAAAAGTAACTGTTCAATCGCAA 924
                                                                                                                                                               805 ATTGCTTACCGTATGAAAGGTAATGAACGTTTTTATTTAATTACCGATGCAATGCGTGCA 864
                                     136 AATGCATTCGAAGGACATGTT 156
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                                                                                                                     16 ATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGATTGACAATGGTGTC 75
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                                                                                                                                                                                                                                                      Score 33.8; DB 10;
Pred. No. 72;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                Length 1182;
                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                    Gaps
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Search completed: March 28, 2003, 17:58:31 Job time : 529 secs

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Title:
Perfect score:
Sequence:
                                                       Result
No.
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Maximum Match 100%
Listing first 45 summaries
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 481.8
445.2
432.6
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                                                       Score
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Match
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Gapop 10.0 , Gapext 1.0
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1161
1 atgatgattcgtcttattgc.....ttcgtccaaatcagaaggca 1161
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 41.5
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 721
638
775
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647
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 12
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BG310598
BF482157
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BG310598 SWOV3MCAM
BF482157 SWOV3MCAM
BF824707 SWOV3MCAM
BF918213 SWOV3MCAM
BF727586 SWOV3MCAM
AII111196 SWOV3MCA1
                                                      Description
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BG310598
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AA625022 SWOV3MCA7 AW313041 SWOV3WCAM BI862949 rm14e03.y	AA618952 SWOV3MCA2 AA625010 SWOV3MCA3 BI781683 kh15h01.y	AA841200 MB3D6AA4G BF918256 SWOV3MCAM AA625024 SWOV3MCA7	AW313040 SWOV3MCAM AW312995 SWOV3MCAM AW288114 SWOV3MCAM	BI783374 kh19b11.y BF400320 SWOv3MCAM AA675020 SWOv3MCA6	BI501509 rm01c11.y AA901444 SWOV3MCAM		AI3ZZU68 SWOV3MCAM AI317885 SWOV3MCAM	BF727629 SWOV3MCAM	AA585626 SW3D9CA34 AA668051 SWOv3MCAM	BF482099 SWOV3MCAM		AA668071 SWOv3MCAM BM284957 kh93a07.v	AI322117 SWOV3MCAM	WOV3MCA1	7	AA/U1/31 SWOV3MCA1	12	85148	BF727527 SWOv3MCAM BF400424 SWOv3MCAM

## ALIGNMENTS

source	FEATURES	ייו ני	শ	н	0		ro:	×	COMMENT	JOURNAL U	TITLE G	AUTHORS W	REFERENCE 1	0	m	ORGANISM C	SOURCE C	KEYWORDS E	VERSION E	ACCESSION B	=	_	DEFINITION S	LOCUS B	
1/21 /organism="Onchocerca volvulus"	Location/Qualifiers	Email: genome@smith.edu	Fax: 4135853786	Tel: 4135853826	College, Northambton, MA, 01063, USA	Department of Biological Sciences, Clark Science Center, Smith	Smith College Department of Biological Sciences	Molecular Parasitology	Contact: Steven A. Williams	Unpublished (1997)	Genes expressed in molting L3 larvae of Onchocerca volvulus	Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.	1 (bases 1 to 721)	Onchocercidae; Onchocerca.	Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;	Onchocerca volvulus	Onchocerca volvulus.	EST.	BG310598.1 GI:13112315	BG310598	mRNA sequence.	(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM55F02 5′,	ŚWOv3MCAM55F02SK Onchocerca volvulus molting L3 larva cDNA	BG310598 721 bp mRNA linear EST 23-FEB-2001	

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GTGAAAGGTCTTTATGATCAAGAAGGTTGCCCGTAATGATGAAGGTGGACGTCAAGTTGCC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 GGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity nes 537; Conserv
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                                                                                                                                                                                                                                                                                                                              GTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAATTCTAAATGCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATCGAGCATATCGAATACAATGCTTTTACATGGAAGCTGATAAGACAGTTAGCGCTCAA 240
                                                                                 GGACAAGAAGCTCACGTCTACAAATATGCGGATCGATCACAACTGTTCTACCAATTTCAA
                                                                                                                                                                                                                 GGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGATTTAATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGAAGTTTCCGAAATGACAACTGCATTTGCAACACAAATTGTACCGATGCCTGTATGC
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                                                                                                                                                                                        GGTTGTGCTTTGGACAAATATTTGCTCAACAACTTGGAATATCCAACTGATTTAATGGCT
                                                                                                                                                                                                                                                                                               GTACATTCATGCTTCGTTGATGATGGTAACGGTGATAAGGTGGAATTATTAAATGCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            slustigm@nybc.org)."
140 c 158 g
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/db_xref="taxon:6282"
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ORGANISM
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377 CTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAACTC
                                                                                                                                                                                               257 GTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTTCGTTTC 316
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                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                          ATCCATTGTTTGTGACAAAAGTTGATCGAGCATATCGAATACAATGCTTTTACATGGAAG
                                                                                                                                                                      GCACGAGGTTCGTTAAATCCCGTGGTATTTTTGTCACATCAGTTGTTGTCATCTCATTCC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
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Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="moiting L3"
//lab_host="XL1-Blue MRF/"
//lab_host="XL1-Blue MRF/"
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 moltlng larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is ~1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
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1 123 c 140 g
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(SL96MLW-OvmL3)"
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/strain="Kumba, Cameroons"
/db_xref="faxon:6282"
/clone="SWOv3MCAM48D12"
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Pred. No. 2.5e-113;
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1 (bases 1 to 775)

Williams, S.A., Lizotte-Waniewski, M., Williams, S.A., Williams, S.A., Williams, Williams, M., Williams, Williams
                                                                                                                                                                                                                                                                                                                                      Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Genes expressed in molting Unpublished (1997) Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onchocerca volvulus Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF824707 775 bp mRNA linear EST 13 SWOVJMCAM52G11SK Onchocerca volvulus molting L3 larva cDNA (SU56MLW-OvmL3) Onchocerca volvulus cDNA clone SWOVJMCAM52
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                                                                                                                                                                                                                                                                             genome@smith.edu
                                                                                  /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOV3MCAM52G11"
/clone_lib="Onchocerca volv:
(SL96MLW-OvmL3)"
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  /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco
Xho I; Filarial nematode parasite of humans. ]
                                           /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                  Location/Qualifiers
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o RI; Site_2:
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larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDH+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E5 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
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Query Match
Best Local Similarity
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                                                                            ATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGGTTGTCCATTCCT 589
                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 469
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CTCACGTCTACCAAT
                       CTCACGTATACAAAT 724
                                                                                                                                                           GCTTCGTTGATGATGGGAAC-GTGATAAGGTGGGAATTATTAAATGCTGTGGGTGTGCCTT
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Best Local :
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                                                                                                                                                                                              CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAAGGTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science Center, College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF918213 758 bp mRNA linear EST 19-JAN-2001 SWOV3MCAM53F10SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWOV3MCAM53F10 5',
                                                                                                                                                                                                                                                                                                                                         Similarity
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/lab_host="XL1-Blue MRF/"
/lab_host="XL1-Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans: Third-stage
larvae, L3, were isolated from infected black files in
Cammeroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2 or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3), 2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(d7) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is -1200 bp. The
library was constructed by Sara Lustigman and Michelle
Lizotte-Wanlewski in the Laboratory of Dr. S. A. Williams.
The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome@smith.edu
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139 c 160 g
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/clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF727586 647 bp mRNA linear EST 08-JAN-2001 SWOV3MCAM51C03SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVmL3) Onchocerca volvulus cDNA clone SWOV3MCAM51C03 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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BF727586.1
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                                                                                                                                                                                                                                                                                                                                                                                                                 4135853826
                                                                                                                                                                                                                                                                                                                                                                       genome@smith.edu
/dev_stage="moiting L3"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
                                                                                                                                                                                                                                              /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                   /clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                            1. .647
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                           /clone="SWOv3MCAM51C03"
                                                                                                                                                                                                                                                                                       /organism="Onchocerca volvulus"
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REFERENCE
AUTHORS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AATTITAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 84.8 nes 452; Conservative
                                                                                                                                                                                                                                                                                                                                                                         GGACCAACCGGTCAACCAGTTCAATTTGCTATCATT--GGTCAGCCAGTTTAT 531
                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTATCTGAAATCACA 420
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                                                                                                                                                                                                                                                                                                                                                           TGCTTTTACATGGAAGCTGACAAAACGGTCAGCACCCAGATCGAAGTGTCCGAAATCACA
                                                                                               Onchocerca volvulus.
Onchocerca volvulus
Eukaryota, Metazoa, Nematoda, Chromadorea,
Onchocercidae, Onchocerca.
Genes expressed in molting Unpublished (1997) Contact: Steven A. Williams Molecular Parasitology
                                                                                                                                                                                                                                     AII11196 665 bp mRNA linear EST 31-AUG-1998 SWOV3MCA1232SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCA1232 5',
                                                                                                                                                                      EST
                                                                 Williams, S.A.,
                                                                                                                                                                                      AI111196.1 GI:3510080
                                                                 (bases 1 to 665)
lliams,S.A., Lizotte-Waniewski,M.,
                                                                                                                                                                                                                     sequence.
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                   Williams
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Pred. No. 1.2e-98;
0; Mismatches 79;
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                                                    larvae
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                                                  Laney, S. and Lustigman, S. of Onchocerca volvulus
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RESULT 6 AI111196

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Query Match
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                        470 TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATTGGTCAGCCAGTTT 529
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                                                                                                                                  CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA 469
                                                                                                                                                                                                           ATCGAATACAATGCTTTTACATGGAAGCTGATNAGACAGTTAGCGCTCAACTTGAAGTTT
                                                                                                                                                                                                                                                            ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT 409
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                                                                                                    CCGAAATGACAACTGCATTTGCAACACAAATTGTCCCGATGCCTGTATGCCGATATGAGA
                                                                                                                                                                                                                                                                                                                   TTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTG
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 4135853786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Camercon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              slustigm@nybc.org)."
1 129 c 136 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2 Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SL96MLW-OvmL3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="SWOv3MCA1232"
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="molting L3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 390.2; DB 9;
Pred. No. 5.8e-98;
0; Mismatches 84;
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CAATTACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCT 266
                                                            CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
Smith Collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.

BE727527

BE727527.1 GI:12045388

EST.
Onchocerca volvulus.
Onchocerca volvulus.
Chromadorea; Spirurida; Filarioidea;
                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome@smith.edu
Seq primer: pBluescript SK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF727527 740 bp mRNA linear EST 08-JAN-20 SWOVJMCAM50EllSK Onchocerca volvulus molting L3 larva cDNA (SU.56MLW-OvmL3) Onchocerca volvulus cDNA clone SWOVJMCAM50Ell 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 4135853786
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and ollgo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Raniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (cmail).
                                                                                                                                                                                                             slustigm@nybc.org)."
a 140 c 157 g
                                                                                                                                                                                                                                       Lizotte-Waniewski in the Laboratory of The library is available from Dr. Sara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SWOv3MCAM50E11"
/clone_lib="Onchocerca volvulus molting L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="molting L3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTTGATGGTGGACCATCCGGAC-ACCTGTTCAATTTGCTACCATTTGGTCAACCAGTG
                                                                                                                                                          TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATTGGTCAGCCAGTTT
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BF400424 648 bp mRNA linear EST 28-NOV-2000 SWOV3MCAM45GllSK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM45Gll 5', Onchocercidae; Onchocerca. Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocerca volvulus Onchocerca volvulus. BF400424.1 mRNA sequence. (bases 1 to 648) GI:11386468

Williams,S.A., Lizotte-Waniewski,M., Genes expressed in molting L3 larvae Unpublished (1997)
Contact: Steven A. Williams Laney, S. and Lustigman, S. of Onchocerca volvulus

Fax: 4135853786

Science

Center,

Smith

il: genome@smith.edu
primer: pBluescript SK. 1. .648 Location/Qualifiers

/strain="Kumba, Cameroons" /db\_xref="taxon:6282" /clone="SWOv3MCAM45G11" /organism="Onchocerca volvulus"

/clone\_lib="Onchocerca (SL96MLW-OvmL3)"

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RESULT 9
BM285148
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                                                       BM285148 646 bp mRNA linear EST 28-DEC-200 kh95c07.yl Ascaris suum L4 pSPORT1 Zarlenga vl Ascaris suum cDNA 5 similar to TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.
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BM285148
BM285148.1 GI:17994190
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GTGCACAGATTGAGGTATCTGAAATCACAACTGCTTTTCAAAACTCAAATTGTCCCGATGC 451
                                                                                                                                                                                                                                                                  AAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGA 271
                                                                                                                                                                                                                                                                                                                                                                         ATGTATACGTGAAGGGACTCTATGATCAAGAGGGATGCCGCAGCGACGACGAGGGTGGACGTC
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                                                                                                      CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA 391
                                                                                                                                                              ATCCTCGTGGTATCTTTGTCACGACGACGGTTGTCATCTCGTTCCATCCGCTCTTCATCA
                                                                                                                                                                                    ATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTA 331
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1 (bases 1 to 646)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,

McCarter, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R.,

Gibbons, M., Ritter, E., Bennett, J., Beck, C., Underwood, K., Steptoe,

Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,

M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,

Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
The library was supplied by Dr. Dante Zarlenga of the USDA
Immunology and Disease Resistance Lab in Beltsville, MD. The
were made from 21 day L4 proximal (isolated from jejunum) and
directionally cloned into the NotI/SalI sites of pSPORT1.
Seq.primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washington Univ. Unpublished (1999)
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Fax: 314 286 1810
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/note="Vector: pSPORT1 (Life Technologies); Site_1: Not1;
/note="Vector: pSPORT1 (Life Technologies); Site_1: Not1;
Site_2: Sal1; The library was supplied by Dr. Dante
Zarlenga of the USDA Immunology and Disease Resistance Lab
in Beltsville, MD. The cDNAs were made from 21 day L4
proximal (isolated from jejunum) and directionally cloned
into the Not1/Sal1 sites of pSPORT1."

173 c 168 g 152 t l others
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/dev_stage="L4"
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/db_xref="taxon:6253"
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0; Mismatches 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes expressed in molting L3 Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, S.A.,
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BG809012.1 GI:14180004
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                                                        /note=""Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note=""Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome@smith.edu
            library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams The library is available from Dr. Sara Lustigman (email:
slustigm@nybc
                                                                                                                                                                                                                                                                                                                                              /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM60E05"
                                                                                                                                                                                                                                                                               /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                (SL96MLW-OvmL3)"
/dev_stage="molting L3"
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d in molting L3 larvae
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of Onchocerca
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          Lustigman (email:
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a volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams,S.A., Lizotte-Waniewski,M., Genes expressed in molting L3 larvae Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                              Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                     AA701731 628 bp mRNA linear ESI 17 DUC . SWOV3MCA1144SK Onchocerca volvulus molting L3 larva cDNA clone SWOV3MCA1144 5',
                                                                                                                                                                                             EST.
Onchocerca volvulus.
                                                                                                                                                                                                                                               mRNA sequence.
AA701731
Smith College Department of Biological Department of Biological Sciences, Clar
                                     Molecular Parasitology
                                                                                                                                          Onchocercidae;
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                      TTATCATAAATGGACATGCGATTCTGAAACC
                                                                                                   TTTTGGATGGTGGACCAACCGGTCAACCAGTTCAATTTGCTATCATTGGTCAGCC--AGT 527
                                                                                                                                               CCGAAATGACAACTGCATTTGCAACACAAATTGTACCGATGCCTGTATGCCGATATGAAA
                                                                                                                                                                   CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGAAA
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                                                           TTCTTGATGGTGGACCATCCGGACAACCTGTTCAATTTGCTACCATTGGTCAACCCAGTG 591
College,
Tel: 4135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oigo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Maniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4135853826
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xho I; Filarial nematode parasite of humans. Third-stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Onchocerca volvulus molting L3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SWOv3MCA1144"
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                                                                                                                                                              CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
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                                                                                                 CAATTACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCT 147
                                                                                                                                                                                                                                                                                                                                                           494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWOV3MCAM45G03SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM45G03 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome@smith.edu
Seq primer: pBluescript
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Department of Biological Sciences, Clark Science Center, Smith
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BF400417
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//dev_stage="molting L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lizotte-Waniewski in the Laboraton The library is available from Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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                                                                                                                                                                                 seq
                                                                                                                                                                                                                            Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                   Onchocercidae; Onchocerca.

1 (bases 1 to 774)

Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)

Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                     BF599177
BF599177.1 GI:11695516
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF599177 774 bp mRNA linear EST 13-DEC-20 SWOV3WCAM49G08SK Onchocerca volvulus molting L3 larva cDNA (SU-6MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3WCAM49G08 5',
                                                                                                                                                                                                                                                                                                                                                                                                          Onchocerca volvulus.
                                                                                                                                                                                 Email: genome@smith.edu
Seq primer: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                4135853786
/organism="Onchocerca volvulus"
/strain="Rumba, Cameroons"
/db_xref="taxon:6282"
/clone="SWOv3MCAM49G08"
/clone_lib="Onchocerca volvulus molt
/clone_lib="Onchocerca volvulus molt
(SL96MLW-OvmL3)"
/dev_stage="molting L3"
/lab host="XL1-Blue MRR'"
/note="Vector: Lambda Uni-ZAP XR; Si
Xho I; Filarial nematode parasite of
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RESULT 14 AA618895 LOCUS

DEFINITION

AA618895 672 bp mRNA linear SWOv3MCA1879SK Onchocerca volvulus molting L3 larva (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3

SWmL3C01879

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                                                                                                                                                                                                                                 TTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTG
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Onchocerca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome@smith.edu
Seg primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Parasitology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onchocercidae;
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/lab_bost="Xil-Blue MRF/"
/notce"Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/notce"Vector: Lambda Uni-ZaP XR; Site_1: Eco Ri; Si
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132 c 129 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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Query Match
Best Local Similarity
Matches 450; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, US
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
The library was supplied by Dr. Dante Zarlenga of the USDA
Immunology and Disease Resistance Lab in Beltsville, MD. Th
were made from 21 day L4 proximal (isolated from jejunum) a
directionally cloned into the Notl/Sall sites of pSPORT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EM284858 612 bp mRNA linear EST 28-DEC-2001 kh99h05.yl Ascaris suum L4 pSPORT1 Zarlenga vl Ascaris suum cDNA 5' similar to TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR.
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Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq
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                                                                                                                /note="Vector: psPoRT1 (Life Technologies); Site_1: NotI; Site_2: SalI; The library was supplied by Dr. Dante Zarlenga of the USDA Immunology and Disease Resistance Lab in Beltsville, MD. The cDNAs were made from 21 day L4 proximal (isolated from jejunum) and directionally cloned into the NotI/SalI sites of psPoRT1."
                                                                                                                                                                                                                                                                                                               /clone_lib="Ascaris suum L4 pSPORT1 Zarlenga v1"
/dev_stage="L4"
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/db_xref="taxon:6253"
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                           31.3%;
75.8%;
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Pred. No. 1.5
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RESULT 16
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                                                                                                                      Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                       AI322117 639 bp mRNA linear EST 22-DEC-1998 SWOV3MCAM12G08SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM12G08 5',
                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                                                                                                                                      Onchocerca volvulus.
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                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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                                                                                                                                                                                                                                                           (bases 1 to 639)
                                                                          primer: pBluescript
                                                                                            genome@smith.edu
   /strain≖"Kumba, Cameroons"
/db_xref≖"taxon:6282"
                                /organism="Onchocerca volvulus"
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                         Onchocerca.
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                                                                                                                                                 Clark Science Center,
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EST.
                                                               AA668071 610 bp mRNA linear EST 20-NOV-19 SWOV3WCAM02C01SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02C01 5',
                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
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/note="Vector: Lambda Uni-ZAP XR;
Xho I; Filarial nematode parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SWOv3MCAM12G08"
/clone_lib="Onchocerca volvulus
(SL96MLW-OvmL3)"
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                   GI:2629570
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Unpublished (1997)
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Department of Biological Sciences, Clark Science Center,
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Molecular Parasitology
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Tel: 4135853826
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/lab_host="XII-Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZaP XR; Site_1: Eco RI; Site_2: Third-Yap XR; Site_1: Eco RI; Site_1: Eco 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    slustigm@nybc.org)."
106 c 138 g
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/clone_lib="Onchocerca v
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/db_xref="taxon:6282"
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BM284957
BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAGTAT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCCAGTTTATCATAAATGGACATGCGATTCTGAAACCGTTGATACTTTCTGCGCGGTT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTAGTAT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Washington Univ. Nematode EST Project, Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Lov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;, mRNA sequence.
BM284957
                                                                                                                                                                                                                                                                                                                                          directionally cloned into the Notl/Sall Seq primer: -40RP from Gibco High quality sequence stop: 500. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Washington Univ. Nematode EST Project, Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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314 286 1810
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                                                                                                                                                                                                                     /dev_stage="L4"
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GGCCAAGAAGCTCACGTATACAAATATGCGGATCGATCACAGCTTTTCTATCAATGCCAG 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: estéwatson.wustl.edu

Email: estéwatson.wustl.edu

The library was supplied by Dr. Dante Zarlenga of the USDA

Immunology and Disease Resistance Lab in Beltsville, MD. The cDNAs

were made from 21 day L4 proximal (isolated from jejunum) and

were made from 21 day L4 proximal (isolated from jejunum) and
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Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R.,
Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,
Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM284957
648 bp mRNA linear EST 28-D kh93a07.yl Ascaris suum L4 pSPORT1 Zarlenga vl Ascaris suum similar to TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PREC
/note-"Yector: PSPORT1 (Life Technologies); Site_1: NotI; Site_2: SalI; The library was supplied by Dr. Dante Zarlenga of the USDA Immunology and Disease Resistance Lab in Beltsville, MD. The cDNAs were made from 21 day L4 proximal (isolated from jejunum) and directionally cloned into the NotI/SalI sites of pSPORT1."
                                                                                                                                                                                                                                                                                                                                                      /organism="Ascaris suum"
/db_xref="taxon:6253"
/clone_lib="Ascaris suum L4 pSPORT1 Zarlenga
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Query Match
Best Local Similarity
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   Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                       BF482126 635 bp mRNA linear EST 06-DEC-20 SWOV3MCAM48B01SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM48B01 5',
                                                                                                           Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                           Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                                                                    Onchocerca volvulus
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EST.
                                                                                                                                                                                                                                                                                                          BF482126
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                                                                                                                                                                                                                                                        Onchocerca volvulus.
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72.3%;
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91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oilgo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
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/clone_lib="Onchocerca volvulus
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/lab_host="XL1-Blue MRF'"
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/db_xref="taxon:6282"
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CCAAAGTTGATCGTGCATATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTA 391
                                                                                                                                                               AAGTTGCCGGAATTTCACTTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGA 271
                                                                                                                                                                                                                            ACGTTTATGTGAAGGGATTGTACGATCAGGAAGGATGTCGAAAACGACGAAAAACGGGCGTA 186
                                                                                                                                                                                                                                                    ATGTTTATGTGAAAGGTCTTTATGATCAAGAAGGTGCCGTAATGATGAAGGTGGACGTC 211
                                                                                                                                                                                                                                                                                                                    TTGAATGTGGACCAACTTCAATAACAATCAATTTAATACACGTAATGCATTCGAAGGAC 151
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                                          ATCCTAGAGGCGTCTTCGTTACTACGACGGTGGTCATCTCATTCCATCCCCTTTTCGTTA 306
                                                                                       ATCCACGTGGTATTTTTGTAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTTGTTA 331
                                                                                                                                    Email: est@watson.wustl.edu
The library was supplied by Dr. Dante Zarlenga of the USDA
Immunology and Disease Resistance Lab in Beltsville, MD. The
were made from 21 day L4 proximal (isolated from jejunum) and
directionally cloned into the NotI/Sali sites of psporT1.
Seq_primer: -40RP from Gibco
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Ascarididae; Ascaris.
1 (bases 1 to 624)
McCarter,J., Clifton,S.,
Dante,M., Marra,M., Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Washington Univ. Nematode EST Project, 1999
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314 286 1810
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/dev_stage="L4"
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/db_xref="taxon:6253"
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Hillier,L., Kucaba,T., Theising,B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
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Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         College, Northampton, MA, Tel: 4135853826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Steven A. Williams
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                                                          /lab_host="XLI-Blue MRF'."

//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture, mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(d1) followed by RNase H and nNa Colt The lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome@smith.edu
                 and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent
                                                                                                                                                                                                                                                                                                                                                                           /clone="SWOv3MCAM47G08"
/clone_lib="Onchocerca volvulus molting L3 larva
                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Kumba, Cameroons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Onchocerca volvulus"
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                                                                                                                                                                                                                                                                                                                                                          (SL96MLW-OvmL3)"
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                                                               Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                             Brugia malayi
Unpublished (1997)
                                                                                                                                                                                                                         Brugia malayi.
Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                    AA585626 776 bp mRNA linear EST 30-DEC SW3D9CA349SK Brugia malayi L3 molting-day 9 larva cDNA (SAW97MLW-BmL3d9) Brugia malayi cDNA clone SW3D9CA349 5', mRNA
                                                                                                                                 Contact: Steven A. Williams
                                                                                                                                                                       Genes expressed in day 9 post-infection,
                                                                                                                                                                                   Williams, S.A. and Lizotte-Waniewski, M.
                                                                                                                                                                                                Onchocercidae; Brugia.
1 (bases 1 to 776)
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                                      Email:
                                                   Fax: 4135853786
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                                    genome@smith.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. William: The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

a 106 c 112 g 180 t
         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362;
Onchocerca volvulus Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                      AA668051 537 bp mRNA linear EST 20-NOV-19 SWOV3MCAM02A04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM02A04 5',
                                                                                        mRNA sequence.
AA668051
                                     Onchocerca volvulus.
                                                                         AA668051.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brugia malayi"
/db_xref="%caxon.6279"
/clone="sw3D9CA349"
/clone=lsw3D9CA349"
/clone=lib="Brugia malayi L3 molting-day 9 larva
(SAW97MLW-BmL3d9)"
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/lab_host="E. coli XL1-Blue MRF/"
                                                                         GI:2629550
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Pred. No. 1.7e-79;
0; Mismatches 63
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Spirurida; Filarioidea;
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                       CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCGTTATGA 467
                                                                                          ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT 409
                                                                                                                                                             TCACATCAGTTGTTCATCCATTCCATTCCATTGTTTTGTGACAAAAGTTGATCGAGCAT 419
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                                                                     ATCGAATACAATGCTTTTACATGGAAGCTGATAAGACAGTTAGCGCTCAACTTGAAGTTT 479
Unpublished (1997)
Contact: Steven A.
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Department of Biological Sciences, Clark Science Center, Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 4135853786
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and objoed of 5010 wed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Libotte-Waniewski in the Laboratory of Dr. S. A. Williams.
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Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black flies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Kumba, Cameroons'
/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _stage="molting L3"
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84.2%;
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Contact: Steven A. Williams
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Department of Biological Sciences, Clark Science Center, Smith
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/lab_host="XLI_Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_2: Eco RI; Site_2:
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127 c 151 g
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 307; DB 12; Pred. No. 1e-74;
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                                                                                                                                                                                                                                                                                                                                       Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI322068 552 bp mRNA linear ES SWOV3MCAM12A04SK Onchocerca volvulus molting L3 larva
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                                                                                                                                                                                                                                                                                                    Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                        Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocerca volvulus.
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Location/Qualifiers
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/dev_stage="moiting L3"
/lab_host="xL1-Blue MRF'"
/lab_host="xL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by
                                                                                                                                        /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
/clone="SMOV3MCAM12A04"
/clone_11b="Onchocerca volvulus
(S196MLW-OvmL3)"
                                                                                                                                                                                                                                 /organism="Onchocerca volvulus"
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cerca volvulus
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AI317885
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Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
                                                                 Unpublished (1997)
Contact: Steven A. Williams
                                                                                              Williams, S.A., Lizotte-Wanlewski, M., Genes expressed in molting L3 larvae
                                                                                                                                                                                  Onchocerca volvulus.
Onchocerca volvulus
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AI317885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  slustigm@nybc.org)."
106 c 111 g
                                                                                                                                                                   Metazoa; Nematoda;
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                                                                                                   Laney, S. and Lustigman, S. of Onchocerca volvulus
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AGATTCTTGATGGNGGACCAATCCG 558
                                                                                                         TATCTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCCGATGCCAGTATGCCCGTTATG 466
                                                                                                                                                                                                              TATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACA--GTTAGTGCACAGATTGAGG 406
                                                                                                                                                                                                                                                      TAACAACAA-CTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATAACAATCTAATTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
                                          AAATTTTGGATGGTGGACCAACCGG 491
                                                                                     TTTCCGAAATGACAACTGCATTTGCAACACAAATTGTACCGATGCCTGTATGCCGATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: $123 of 123 of 180 the constructed in the laboratory of Dr. S. A. Williams.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome@smith.edu
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(SL96MLW-OvmL3)"
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/clone="SWOv3MCAM06H12"
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/strain="Kumba, Cameroons"
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                                                                                                                                                                               GGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCACTTCCATTTGATTCA 243
                                                                                                                                                                                                                                                               TITAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAA 183
                                                                                                                                                                                                                                                                                                                                               ATGATTCGTCTTATTGCTTTCTGTACTACACTTATTGCATTGTCTTATTCGATTCCGGTT 63
                GTCATTTCGTTTCATCATTATTTGTTACCAAAGTTGATCGTGCATATCGAGTACAATGC 363
                                                                                                                                                                                                                                                                                                                                                                                                        ATGCTTCGTCTTACCGCTCTTTGTGCTACTCTTTTCGCGGTGTCATATGCAATTCCTGTT 149
GTAATTTCCTTCCATCCACTGTTCGTCACAAAAGTTGATCGAGCATACCGAGTGCAGTGC
                                                                                                                      TGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTGTAACAACAACTGTT 303
                                                                                                                                                                                                                                          TTCAATACACGTAATGCATTCGAGGGACACGTTTACGTGAAAGGTCTTTACGATCAAGAA 269
                                                                                                                                                              GGCTGCCGTAACGATGAGGGTGGACGTCAGGTCGCTGGAATTTCACTTCCTTTTTGATTCC
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BE758436 BE758436.1 GI:10172428
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
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Unpublished (1999)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams, S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from young adult worms isolated from the peritoneal cavity of jirds and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNASE H and DNA pol I. The library has 6.5 x 104 independent recombinants and the average insert size is approx. 800bp. The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr. S.A. Williams, email: genome@neal.smith.edu." a 119 c 123 g 159 t
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/clone="SWYACAL10F01"
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/lab_host="XL1-Blue MRF'"
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ATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
Contact: Steven A. Williams
Molecular perceits
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                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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//lab_host="XLL-Blue 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome@smith.edu
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/db_xref="taxon:6282"
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                                                                                          Score 297.6; DB 10,
Pred. No. 4.3e-72;
Pred. No. 4.3e-72;
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                                                                                                                                            DB 10;
                                                                                               Indels
                                                                                                                                            Length 694;
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540 AGAATCTTGGATGGTGGACCCATCCCGGACAAACCTGTTCAATTTGCTACCCATTG
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                                                                                                                                                                                                                     The library was constructed by Brandi Chiapelli and Dr. James (bchiapel@watson.wustl.edu) at (bchiapel@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Nematodes were provided by Dr. David Bird and Daniel Snyder of North Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 534)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Marter, J., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, T., Kennedy, S., Maguire, L., Beck, C., Onderwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 bp mRNA linear EST 29-AUG-2001 rm01cl1.yl Meloidogyne arenaria egg pAMP1 v1 Chiapelli McCarter Meloidogyne arenaria cDNA 5' similar to TR:018479 018479 CUTICLIN-1. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                             High quality sequence stop: 378
Location/Qualifiers
                                                                                                                                                                                          State University.
                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Washington Univ. Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
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                              /organism="Meloidogyne arenaria"
/db_xref="taxon:6304"
/clone_lib="Meloidogyne arenaria egg
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pamp1 v1 Chiapelli
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VERSION
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JOURNAL
                      TITLE
                                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGAAGCTCACGTTTATAAATATGCTGATCGTTCACAACTTTTCTATCAATGCCAAATT 360
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                                                   Onchocercidae; Onchocerca.

1 (bases 1 to 531)
Williams,S.A., Lizotte-Waniewski,M., Laney,S., Lustigman,S.,
Hilliams,J., Allen,M., Bowles,L., Geisel,S., Jost,S., Kucaba,T.,
Hillier,L., Allen,M., Theising,B., White,Y., Wylie,T., Chappell,J.,
Martin,J., Steptoe,M., Theising,B., White,Y., Wylie,T., Chappell,J.,
Person,B., Gibbons,M., Harvey,N., Pape,D., Chamberlain,A.,
Morales,R., Schurk,R., Ritter,E., Kohn,S., Underwood,K. and Marra
                                                                                                                                                                                                                                                                                                                                           AA901444
531 bp mkNA ILHEGI CU. .... AA901444
SWOV3MCAM03B05 Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OVML3) Onchocerca volvulus cDNA clone onch17 5' similar to TR:Q93115 Q93115 CUT-1-LIKE CUTICLIN PROTEIN PRECURSOR. ;, mRNA
Unpublished (1998)
                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                     Onchocerca
                                                                                                                                                                                                                                                           Onchocerca volvulus.
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76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 ATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                              CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
TAACAACAACTGTTGTCATTTCGTTTCATCCATTATTTGTTACCAAAGTTGATCGTGCAT 349
                                                                                                                                                                                                                           TTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTG
                                                                                                                                                                                                                                                                                                   TATACGATCAGGCAGGATGCGNNAATGATGAAGGTGGACGTCAGGTAGCCGGAATTGAAC
                                                                                                                                                                                                                                                                                                                            TTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCAC 229
                                                                                                                                                                                                                                                                                                                                                                                                     CAATTACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATGTATACGTGAAAGGCT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCTATTCCGGTTGATAACGGTGTAGAAGGTGAACCAGAAATTGAATGTGGTCCAACAT 196
                                                                                                                                                                                                 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S.A.Williams. The Lizotte-Waniewski in the Laboratory of Dr. S.A.Williams. The library is available from Dr. Sara Lustigman email slustigm@enybc.org When requesting this clone from Dr. Lustigmplease reference the Williams lab clone id - SWOV3MCAM03B05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and ollgo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda UN1-Zap XR vector and has 1 x 1026 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Libotte-Waniewski in the Laboratory of Dr. S. A. Williams.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  נם
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            slustigm@nybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The library is available from Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="XL1-Blue MRF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Onchocerca
/strain="Kumba, Camerc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Onchocerca volvulus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SL96MLW-OvmL3)"
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Pred. No. 2.4e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ascarididae; Ascaris.

1 (bases 1 to 592)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,

Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R.,

Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe

M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,

Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1783374 592 bp
kh19b11.y1 Ascaris suum female g
Ascaris suum cDNA 5' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washington Univ. Nematode EST Project,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ascaris suum
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                                                                                                                    165
    Conservative
                                                                                                             were provided by Dr. Alan Scott (ascott@jhsph.edu) of the School of Public Hygene and Public Health at John Hopkins University in Baltimore, MD."

136 c 135 g 156 t
                                                                                                                                                                                                  /note="Vector: pAMP1 (Gibco); Site_1: Not1; Site_2: Sal1; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues
                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Dissected
most proximal region of
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Ascaris suum female gonad Chiapelli McCarter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Ascaris suum"
/db_xref="taxon:6253"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                       24.5%;
75.9%;
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                     Score 285; DB 13;
Pred. No. 1.3e-68;
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gonad MZ pAMPl v2 Chiapelli I
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                                                                                                                                                                                                                                                                                                                                                          Williams, S.A., Lizotte-Waniewski, M., Genes expressed in molting L3 larvae Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF400320 622 bp mRNA linear EST 28-NOV SWOV3MCAM44H03SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM44H03
                                                                                                                                                                                                                                                                                             Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BF400320
                                                                                                                                                                                                                                                  Fax: 4135853786
                                                                                                                                                                                                                                                                            Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocerca volvulus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 622)
                                                                                                                                                                                                     primer:
                                                                                                                                                                           genome@smith.edu
imer: pBluescript SK.
Location/Qualifiers
                                                                                     /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                     (SL96MLW-OvmL3)"
                                        /clone_lib="Onchocerca
                                                                /clone="SWOv3MCAM44H03"
                                                                                                                                  /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:11386388
                                          volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Laney, S. and Lustigman, S. of Onchocerca volvulus
                                      molting
                                        L3
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BASE COUNT ORIGIN

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Query Match Best Local Similarity

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TTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGCAACTTCGT 885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGATTGAAATAAGCGAACAGAATCCGAACCTATCAGCTAAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGAT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCTCAAGAAGCGATCGGTTAATTATGATAATACGGTGGATGTTAGTGCCGGTTTTAGC
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                                                                                                                                                                                                                            AA625020
363 bp mRNA linear EST 12-NOV-199 SWOV3WCA691SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C0691 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately do nolting larvae (mL3),2000 larvae from day 1, 2 or 3
volvulus.
volvulus
Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                         GI:2537422
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Pred. No. 2.6e-
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                                                                        TTTAATGGCTGGACAAGAAGCTCACGTCTACAANTATGCGGATCGATCACAACTGTTCTA 360
                                                                                                                                                                                                                                                                                                                                                                                                    CTGCGCGGTTGTCCATTCCTGCTTTGTCGATGATGGTAACGGTGATACTGTGGAAAATTCT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCATTGGTCAACCAGTGTACCATAAATGGACATGTGATTCTGAAACAGTTGATACATT
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                                                                                                                                                                                                                                  AAATGCTGATGGATGTGCTCTTGATAAATATTTGCTAAATAATTTGGAATATCCAACAGA 689
                                                                                                                                  Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
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Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome@smith.edu
Seq primer: pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onchocercidae; Onchocerca.
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10; Conservative
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/db_xref="taxon:6282"
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Pred. No. 6e-67;
0; Mismatches 53;
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126 TAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTCTTTATGATCAAGAAGG
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                                                                                                                                                                                                                                                               Local Similarity
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SWOV3MCAM38A02SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM38A02 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Contact: Steven A. Williams
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                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: /note="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Raniewski in the Laboratory of Dr. S. A. Williams.
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                                                                                                                                                                                                                                                                                                                                                           slustigm@nybc.org)."
111 c 114 g
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/clone_lib="Onchocerca volvulus molting L3
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/db_xref="taxon:6282"
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SWOV3MCAM37E11SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM37E11 5',
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
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Williams, S.A., Lizo
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               /note-"Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in cameroon (forest strain). The L3 were cultured in 20% FCS in INDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
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/db_xref="taxon:6282"
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/clone_lib="Onchocerca volvulus molting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCGAATACAATGCTTTTACATGGGAGCTGATAAGACAGNTAGCGCTCAACTTGGAAGT
                                                                                                                                                                                                                                                     Onchocercidae; Onchocerca.

1 (bases 1 to 577)

Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                                                                  Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW288114 577 bp mRNA linear EST 16-JAN-20
SWOyJMCAM33H10SK Onchocerca volvulus molting L3 larva cDNA
SWOyJMCAM33H10SK Onchocerca volvulus cDNA clone SWOyJMCAM33H10 5',
                                                                                                                                                               College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                        Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW288114
AW288114.1 GI:6695049
                                                                                                                       Fax: 4135853786
                                                                       primer: pBluescript
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                                                                                               genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      മ
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104 c 110 g 166 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has I x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams.
/organism="Onchocerca volvulus"
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reverse transcriptase and oligo(dT) followed by RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                     volvulus
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Pred. No. 5.
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.72; Indels
                                                                                                                                                                                         Clark Science Center,
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Onchocercidae; Brugia.

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                                                                                                                                                                                                                                                                                                                                                                  521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 ATTCGATTCCGGTTGACAATGGTGTCGAAGGTGAGCCAGAAATTGAATGTGGACCAACTT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAATAACAATCTATTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
                                                                                                                                                                                                                                                                                                                                                                CCGAAATGCCACTGGCATTTGCAACACAAATTGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                CTGAAATCACAACTGCTTTTCAAACTCAAATTGTCCC 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATTGAGGTAT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCAC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACATCAGTTGTTGTCATCTCATTCCATCCATTGTTTGGGACAAAAGTTGATCGAGCAT
                                                                                                                                                                                AA841200 354 bp mRNA linear EST 02-MAR-1998 MB3D6AA4G10T3 Brugia malayi day 6 post-infection third stage larvae SAW96MLW-BmL3d6 Brugia malayi cDNA clone 3D6AA4G10 5', mRNA
Brugia malayi.
Brugia malayi
Eukaryota; Metazoa; Nematoda;
                                                                                EST.
                                                                                                        AA841200
AA841200.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        larvae, 13, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1026 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Library is available from Dr. Sara Lustigman (email: slustigménybc.org).*

78 a 118 c 108 g 173 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="SWOv3MCAM33H10"
/clone_lib="Onchocerca volvulus molting L3 larva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SL96MLW-OvmL3)"
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     Chromadorea;
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  Spirurida;
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                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                 638 ATGGATGTGCTCTTGATAAATATTTTGCTAAATAATTTGGAATATATCCAACAGATTTAATGG
                                                                                                                                                                                                                    121 AGATCAGTATCACTATTAAAGAACCAAACAGTGAATGTGCTCGGCCACAATGTTCAGAGC
                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                     1 ATGGTTGTGCTCTCGACAAATATTTGCTAAACAATTTGGAATATCCAACGGATCTTATGG
                                                                                         AACTTCGTTTACTCAAGAAAAGATCTGCAGAACCGGAGAATATCATTGATGTACGAACTG
                                                                                                                                                                CACAAGGATTCGGAGCTGTTAAAACAGGTGGTGCCGCAGCAAAACCTGCTGCAGCTGCGC
                     ATATCAACACCCTTGAAATTAGCGATGATAATCAAGCTTTGCCAGTTGATTTAC
ATATCAGCGCCCTTGAAATCATCGAAGACAATCAAGCTCTACCAGTTGACTTGC 354
                                                                                                                                             CGCAAGGATTTGGAGCTGTTAAAACGGGAGGTGCCGCAGTTAAACCTGCAGCAGCTGCTC
                                                                                                                                                                                                                                         AGATCAGTATTACCATTAAAGAACCAAATAGCGAATGTGTGTCGACCACAATGTTCAGAAC
                                                                    AGCTCCGCTTGCTCAAGAAAAGGTCTGCGGAACCAGAGAACGTCGTCGACGTGAGGACTG
                                                                                                                                                                                                                                                                                              301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 354)
Blaxter, M.L., Water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The ABI trace of this sequence can be viewed at http://www.sanger.ac.uk/brugia/3D6/MB3D6AA4G10T3.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes expressed in day six post-infection, third stage larvae of Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Jones, S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +44 131 650 6760
+44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 2 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Michelle Lizotte-Waniewski. The library is available from The Filarial Genome Project Resource Center: contact Dr. S.A. Williams, Clark Science Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu." a 81 c 84 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: lambdaZapII (UniZap XR); Site_1: Eco R I (5' end); Site_2: Xho I (3' end); Brugia malayi is a lymphatic filarial nematode parasite of humans. mRNA was prepared from third stage larvae of Brugia malayi isolated from the peritoneal cavity of jirds six days after infection. The mRNA was converted to double stranded cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Brugia malayi day 6 post-infection third stage
larvae SAW96MLW-BmL3d6"
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/strain="TRS Labs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 269.2; DB 9
Pred. No. 2.9e-64;
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Matches 332
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Contact: Steven A. Williams
Molecular Parasitology
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Location/Qualifiers
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Department of Biological Sciences, Clark Science Center, Smith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cameroon (forest strain). The L3 were cultured in 20% FCS in INDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture, mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNAse H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Library was constructed by Sara Lustigman and Michelle Library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."

95 a 139 c 152 g 217 t 2 others
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/note-"Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
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/db_xref="taxon:6282"
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 269.2; DB 1
Pred. No. 3.7e-64;
0; Mismatches 70
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Onchocerca volvulus.
Onchocerca volvulus
Chromadorea; Spirurida; Filarioidea;
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
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Unpublished (1997)
Contact: Steven A. Williams
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Williams, S.A., Lizotte-Waniewski, M.,
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    Location/Qualifiers
                                                                                /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oilgo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Wanlewski in the Laboratory of DT. S. A. Williams.
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                 The library is available from Dr. slustigm@nybc.org)."

91 c 93 g 144 t 1:
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(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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                    12 others
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                                                              Sara Lustigman (email:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCATTTGATTCATGCAATGTTGCGCGTACACGATCTCTGAATCCACGTGGTATTTTTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAATAACAATCAATTTTAATACACGTAATGCATTCGAAGGACATGTTTATGTGAAAGGTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCAC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATTACTGTCAACTTTAATACTCGTAATCCATTTGAAGGACATNTNTACGTGAAAGGCT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGAAATGACAACTGCAT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCGNTTGATTCCTGTAATGTAGCACGTACACGTTCGTTANNTCCACGTGGTATTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCACATCAGTTGTTGTCATCTCATNCCATCCATTGNTTGTGACAAAAGTTGATCGAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA618952
459 bp mRNA linear EST 12-NOV-1997 SWOV3MCA2020SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO2020 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Steven A. Williams
Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams, S.A., Lizotte-Waniewski, M., Laney, S. and I Genes expressed in molting L3 larvae of Onchocerca Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onchocerca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA618952.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer: pBluescript
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/dev_stage="moiting L3"
/lab_host="XL1-Blue MRF'"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Eco RI; Site_2
                                                                                                                                                                                                           /clone="SWmL3CO2020"
/clone_lib="Onchocerca volvulus molting L3
(SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                         /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           volvulus.
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80.7%;
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Pred. No. 7.8e-64;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                larva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328
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Search completed: March 28, 2003, 16:58:33 Job time: 1655 secs
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.7
Best Local Similarity 83.9
Matches 296; Conservative
                                                                                                                                                 350 ATCGAGTACAATGCTTTTACATGGAAGCTGATAAAACAGTTAGTGCACAGATT 402
                                                                                                                                                                                                                                201 TATACGATCAGGCAGGATGCCGAAATGATGAAGGTGGACGTCAGGTAGCCGGAATTGAAC
                                                                                                                                                                                                                                                                                                                                    170 TITATGATCAAGAAGGTTGCCGTAATGATGAAGGTGGACGTCAAGTTGCCGGAATTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. I3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10E6 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmenybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 263; DB 9; Length 459; Pred. No. 1.7e-62; O; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being
1086.5
1086.5
776.5
776.5
199
166
163
162.5
                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                       re greater than or equal to the score of the result bein is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                   Query
Match
  100.0
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1 MMIRLIAFCTTLIALSYSIP.....ALIAAVIITISFKFRPNQKA 387
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980 DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981 DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982 DAT: *
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983 DAT: *
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                                                                                                                                                                                                                                                                      Length
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     IJ
ABB67889
ABB67239
                                             AAB84258
ABB76278
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ABB59975
ABB59061
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                                                                                                                                          Amino acid sequenc
Dirofilaria immiti
Amino acid sequenc
Brugia malayi cuti
                                                                                                                                                                                                                                                                 Description
                 Drosophila melanog
Drosophila melanog
Drosophila melanog
                                                                                             Amino acid sequenc
Dirofilaria immiti
                                                                                                                                                                                                                                                                                                                                                                                                                printed,
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84	85.5	85.5	85.5	85.5	85.5	85.5	85.5	86.5	86.5	86.5	87	87	87	87.5	87.5	90	92	93	94.5	94.5	94.5	97	100	100.5	111	119.5	124.5	130.5	135.5	140	142	150	162.5
4.1	۰. د د		4.2	•									4.3	4.3		4.4	4.5				4.7		4.9										
474	1121	1120	1118	1117	940	560	438	747	747	636	3038	473	473	474	474	2515	896	474	875	875	693	227	935	768	2284	418	699	638	744	692	833	758	611
22	) N	22	23	23	22	18	23	22	22	22	16	21	21	21	21	22	23	22	16	10	10	22	13	22	22	22	22	22	22	22	22	22	22
AAB94481	AAM41222	ABG10284	026	AAU78053	AAM39436	AAW13009	ABP38294	AAB93124	AAM40070	AAB94352	AAR74171	AAY70924	AAY70901	AAY70923	AAY70900	ABB64427	ABB08760	ABB63130	AAR73053	AAP94854	AAP94856	ABB71814	AAR20112	ABB68660	ABB71434	ABB68164	ABB64367	ABB64380	ABB58426		ABB58185	5833	ABB70054
	Human polypeptide	human diagn	lung specif	desmoglein	Human polypeptide	Segment of desmoso	Staphylococcus epi	Human protein sequ	Human polypeptide	Human protein sequ	Aspergillus terreu	Human soluble CD39	Protein encoded by	Human soluble CD39	Protein encoded by	Drosophila melanog	Synechococcus cyan		•		Expression plasmid	ila	—									Drosophila melanog	Drosophila melanog

## ALIGNMENTS

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RESULT 1
AAB84258
WPI; 2001-396953/42.
N-PSDB; AAH24826, AAH24828.
                                                   Chandrashekar R, Morales
                                                                                         01-JUN-1998;
                                                                                                       01-JUN-1999;
                                                                                                                      19-JUN-2001.
                                                                                                                                      US6248329-B1.
                                                                                                                                                    Dirofilaria immitis.
                                                                                                                                                                  Cuticlin; gene therapy; vaccine; helminth parasite
                                                                                                                                                                                  Amino acid sequence of a cuticlin polypeptide
                                                                                                                                                                                                  22-AUG-2001
                                                                                                                                                                                                                 AAB84258;
                                                                                                                                                                                                                               AAB84258 standard; Protein; 387 AA
                                                                 (MORA/)
                                                                         (CHAN/) CHANDRASHEKAR R.
                                                                  MORALES T H.
                                                                                                                                                                                                 (first entry)
                                                                                         98US-0087435
                                                                                                        99US-0323427.
                                                   TH;
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Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin protein is useful as a vaccine to prevent parasitic helminth infection

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RESULT 2
ABB76278
ID ABB7
XX ABB7
XX ABB7
XX D1rc
XX D1rc
XX Cuti
KW anth
XX anth
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Best Local S
Matches 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin may all be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover desired proteins. They may also be used to target cytotoxic agents to the parasite and kill it directly. The present sequence represents a cuticlin
  20-MAR-2001; 2001US-0812642
                            28-MAR-2002
                                                    US2002037294-A1
                                                                            Dirofilaria immitis
                                                                                                         anthelmintic.
                                                                                                                       Cuticlin;
                                                                                                                                              Dirofilaria immitis
                                                                                                                                                                        12-AUG-2002
                                                                                                                                                                                                 ABB76278;
                                                                                                                                                                                                                           ABB76278 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                                                                                               301
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                                                                                                                                                                                                                                                                                          MFMGLSIALIAAVIITISFKFRPNOKA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMIRLIAFCTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQ
                                                                                                                                                                                                                                                                                                                                           SAEPENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFS
                                                                                                                                                                                                                                                                                                                                                                                               KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFYMEADKTVSAQIEVSEITTAFQTQIVFMPVCRYEILDGGFTGQFVQFAIIGQFVYHKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCDSETVDTFCAVVHSCFVDDGNGDTVETLNADGCALDKYLLNNLEYPTDLMAGQEAHVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
387; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Column
                                                                                                                   helminth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39-40;
                                                                                                                                                                                                                            Protein;
                                                                                                                                              cuticlin
                                                                                                                                                                       entry)
                                                                                                                   parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29pp; English.
                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0:
                                                                                                                                             DiCut-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2026; DB 22; Pred. No. 7.1e-210;
                                                                                                                    DiCut-1A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                 vaccine; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 3 AAB84260

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AAB84260; 22-AUG-2001

(first entry)

AAB84260

standard;

Protein;

245

360 360 300 300 240 180

240

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated cDNA clone (see ABL57372). The protein sequence has 918 identity to the Ascaris homologue. The invention provides D. immitis and Brugia malayi parasitic helminth cuticlin proteins, nucleic acids, antibodies, compounds that inhibit cuticlin activity, and methods of obtaining them. Therapeutic compositions comprising such proteins, nucleic acids, antibodies and/or inhibitors, including genetic vaccines, recombinant virus vaccines and recombinant cell vaccines, are used to protect animals from diseases caused by parasitic helminths, and to inhibit the moulting of filariid larvae in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the protein sequence of novel Dirofilaria immitis cutillin DiCut-la, as predicted from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New parasitic helminth cuticlin proteins and nucleic acids isolated form Dirofilaria immitis, useful for protecting animals from diseases caused by parasitic helminths or for inhibiting molting of filariid larvae in an animal -
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chandrashekar R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1999;
361
                          361
                                                     301
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                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHAN/)
                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                 1 MMIRLIAFCTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQ
             MEMGLSIALIAAVIITISEKERPNQKA 387
                                                                 SAEPENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFS
                                                                                                                        KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKR
                                                                                                                                                              SAEPENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFS
                                                                                                        KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKR
                                                                                                                                                                                                                                                                                          EGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQ
                                                                                                                                                                                                                                                                             EGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQ
                                                                                                                                                                                                                                                                                                                                   MMIRLIAFCTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-401306/43.
DB; ABL57372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Page
                                                                                                                                                                                                                                                                                                                                                                                          387;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHANDRASHEKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                387
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ŘΑ;
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                       Score 2026; DB 23;
Pred. No. 7.1e-210;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                   387;
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Best Local S
Matches 195
                                                                                                                                                                                                                                                                                                                                                                 The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin may all be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover desired parasite and kill it directly. The present sequence represents a cuticlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid molecule encoding a Dirofilaria immitis cuticlin protein is useful as a vaccine to prevent parasitic helminth infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 53-54; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chandrashekar R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brugia malayi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuticlin; gene
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHAN/) CHANDRASHEKAR R. (MORA/) MORALES T H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a
 244
                         242
                                                      184
                                                                               182
                                                                                                          124
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                                                                 CDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYK 241
                                                                                                                       FYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWT 181
                                                                                                                                                                                                                    2001-396953/42.
DB; AAH24839.
ΥA
                                                                                                         FYMEADKTVSTQIEVSEMTTVFATQLVPMPVCRYEILDGGPTGQPVQYANIGQPVYHKWT
                                                                                                                                                               DCRSDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTAVVVITFHPQFITKVDRTYRLQC
                                                                                                                                                                             GCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQC 121
                                                    CDSETVDTFCALVHSCFVDDGNGDSINLINEEGCALDRYLLNNLEYPTDLMAGQEAHVYK
                           YA 243
                                                                                                                                                                                                                                                                          al Similarity
195; Conserv
 245
                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy;
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                                                                                                                                                                                                                                                                                       53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cuticlin polypeptide
                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                       Score 1086.5;
Pred. No. 1.3
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  helminth parasite.
                                                                                                                                                                                                                                                                                       .3e-108;
                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                    22; Length
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                    245;
                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                       cuticlin
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RESULT 4 ABB76280

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YA 243

184

122

FYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQEAIIGQPVYHKWT 181

FYMEADKTVSTQIEVSEMTTVFATQLVPMPVCRYEILDGGPTGQPVQYANIGQPVYHKWT

183

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64

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Qy
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                                                                    Q
                                                                                                                                              Query Match
Best Local :
                                                                                                Matches
                                                                                                                                                                 The present sequence is the protein sequence of novel Brugia malayi cuticlin BmCut-lA, as predicted from an isolated partial CDNA clone (see ABL57374). The invention provides B. malayi and Dirofilaria immitis parasitic helminth cuticlin proteins, nucleic acids, antibodies, compounds that inhibit cuticlin activity, and methods of obtaining them. Therapeutic compositions comprising such proteins, nucleic acids, antibodies and/or inhibitors, including genetic vaccines, recombinant virus vaccines and recombinant cell vaccines, are used to protect animals from diseases caused by parasitic helminths, and to inhibit the moulting of filariid larvae in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHAN/)
(MORA/)
                                                                                                                                                                                                                                                                                                                                      New parasitic helminth cuticlin proteins and nucleic acids isolated form Dirofilaria immitis, useful for protecting animals from disease caused by parasitic helminths or for inhibiting molting of filariid larvae in an animal
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                 Example 1; Page 28-29; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chandrashekar R, Morales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002037294-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cuticlin; helminth; parasite; BmCut-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brugia malayi cuticlin BmCut-1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76280 standard; Protein;
                          62
                                               2002-401306/43.
DB; ABL57374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHANDRASHEKAR R.
MORALES T H.
                                                                                                          Similarity
                                                                                                                                             245 AA;
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0812642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0323427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                          53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TH;
                                                                                                .24;
                                                                                               Score 1086.5;
Pred. No. 1.3e
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                          .3e-108;
                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy;
                                                                                                                     Length
                                                                                                                     245;
                                                                                               1;
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AAB84259
                                                                                                                                                                                                            Matches 144;
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                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                  The specification describes a Dirofilaria immitis nucleic acid molecule, that encodes a cuticlin protein. The Dirofilaria immitis nucleic acid molecule is useful as a probe to identify nucleic acid molecules, as a primer to produce nucleic acids, as a therapeutic reagent, e.g., gene therapy to inhibit cuticlin activity or production, or in a vaccine to prevent infection with helminth parasites. The cuticlin protein, antibodies raised against it, and inhibitory compounds of cuticlin may all be used in compositions to protect animals, especially mammals such as cats, dogs, and humans. The antibodies may be used to passively immunize an animal, or as reagents in assay to detect infection of helminths, or as tools to screen expression libraries to recover desired parasite and kill it directly. The present sequence represents a cuticlinarion contains.
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                              polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule encoding a Dirofilaria i protein is useful as a vaccine to prevent parasitic
              305
                                                                                                                                               Example 1; Column 47-50; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH24830, AAH24832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dirofilaria immitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cuticlin; gene therapy; vaccine; helminth parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a cuticlin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB84259 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHAN/) CHANDRASHEKAR R. (MORA/) MORALES T H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-2001
                                                                                                                          194
                                                                                                                                                                                                                         Local Similarity
ENIIDVRTDINTLEISDDN
                                                                                                          VHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQ
                                                     ISITIKEPNSECVRPQCSEPQGFGAVKTG-----GAAAKPAAAAQL----RLKKRSAEP
                                                                                         VHSCVVDDGKGDAVEILNEEGCALDKYLLNNLEYITDLMAGQEAHVYKYADRSELYYQCQ
                                     ISITIKEPHSECPRPQCTEPQGFGAIKSGQGFAAVKSAAAPAPEASLLSPRLIKKRSINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-396953/42.
                                                                                                                                                                                                                                                                  271 AA;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0087435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9908-0323427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morales TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                      38.3%;
           323
                                                                                                                                                                                                          24;
                                                                                                                                                                                                      Score 776.5; DB 22;
Pred. No. 4.8e-75;
4; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dirofilaria immitis cuticlin ent parasitic helminth infect
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                    271;
                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
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ABB76279
                                                                                                                                                                                           Query Match
Best Local S
Matches 144
                                                                                                                                                                                                                                                                        The present sequence is the protein sequence of novel Dirofilaria immitis cuticlin Dicut-1B, as predicted from an isolated cDNA clone (see ABL57373). The protein sequence has 81% identity to the Ascaris homologue. The invention provides D. immitis and Brugia malayi parasitic helminth cuticlin proteins, nucleic acids, antibodies, compounds that inhibit cuticlin activity, and methods of obtaining them. Therapeutic compositions comprising such proteins, nucleic acids, antibodies and/or inhibitors, including genetic vaccines, recombinant virus vaccines and recombinant cell vaccines, are used to protect animals from diseases caused by parasitic helminths, and to inhibit the moulting of filariid larvae in an animal.
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 25-26; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New parasitic helminth cuticlin proteins and nucleic acids isolated form Dirofilaria immiltis, useful for protecting animals from diseases caused by parasitic helminths or for inhibiting molting of filariid larvae in an animal .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-401306/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chandrashekar R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dirofilaria immitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuticlin;
305
                            135
                                                       254
                                                                                                            194
                                                                                                                                                                  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL57373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHAN/) CHANDRASHEKAR
(MORA/) MORALES T H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dirofilaria immitis cuticlin DiCut-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           АВВ76279;
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                                                                                 75
                                                                                                                                       15
                                                                             VHSCFVDDGNGDTVEILNADGCALDXYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQ
                                                                                                                                    IEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAV 193
ENTIDVRTDINTLEISDDN 323
                         ISITIKEPHSECPRPQCTEPQGFGAIKSGQGFAAVKSAAAPAPEASILSPRLIKKRSINS
                                          ISITIKEPNSECVRPQCSEPQGFGAVKTG-----GAAAKPAAAAQL---RLLKKRSAEP
                                                                                                                                                                                           144;
                                                                                                                                                                                         h 38.3%; Score 776.5; DB 23
Similarity 72.4%; Pred. No. 4.8e-75;
44; Conservative 24; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          helminth;
                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; gene therapy;
                                                                                                                                                                                                                  23;
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                                                                                                                                                                                          9;
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RESULT 7
ABB59975
ID ABB5
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences (ABL0184)
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
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                                                                          175 YLRKHAQKPQAFRSDDRREYGRSLDKQQDDDLDEEDVYDANAPTQEEDVT----NNEIPM
                      151 PVC-----RYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
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                                                                                                                                                                                YKLPLRSCN-TMPKETDDGGIEFFNTIVLQPHLKLITDLGRGYHVRCAYKSRDAAMKPKK 174
                                                                                                                                                                                                                             ISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTV----
                                                                                                                                                                                                                                                                                                                                           VEGEPEIEC -- GPTSITI ---- NFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAG ---
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                                                                                                                                                                                                                                                                                          VEPSVRIKCLSGSMLITIKDAPPNHET-GLFSGMIYPKGLSKNSTCLSEY--RDHVGSLR 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 AA
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6717; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-191637P.
2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                          Score 199; DB 22,
Pred. No. 3e-12;
"" matches 150;
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RESULT 8
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                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10151-ABL30511), expressed DNA sequences (ABL01040-ABL16175) and the encoded proteins
                                 The sequence data for this patent did not form specification, but was obtained in electronic i
Sequence
                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                            Disclosure; SEQ ID NO 36975; 21pp + Sequence Listing; English.
                                                                                                                                                                                                       interactions
                                                                                                                                                                                                                 New isolated nucleic a
                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                               Venter JC,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 36975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB70061;
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DB; ABL14164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NENENAN-----DSDEDAVYKEK------TLDDALCVSQRTFAIAIAIAGLILMLAVVA 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-DTVEILNADGCALDKYLLNNLEYPTDLMAGQ---EAHVYKYADRSQLFYQCQISITIK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGCHMKIYNDEHKIADDVKIGDPLTIVI-----SIDKQKV--YGLHVTDCIVRDGL
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604
                                                                                                                                                                                                                                                                                               Adams
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2000US-0614150.
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                                                                                                                                                                                                                 detection reagent for detecting for elucidating cell signalling
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format directly from
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Query Match Best Local S Matches 72

Similarity 72; Conserv

8.2%; ilarity 22.0%; Conservative !

54;

Score 166; DB 22; Pred. No. 1.7e-08; 4; Mismatches 135

135;

66;

Gaps

17;

Length 604; Indels

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RESULT 9
ABB67889
AD AB67889
AD AB67889
AX AB66
AX AB66
AX AB66
AX AB66
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                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL13511), expressed DNA sequences (ABL16175, and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.0%;
19.8%;
                                                                                                                Li
                                                                                                                PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
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Pred. No. 1.8e-07;
                                                                                                             Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128;
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New isolated nucleic

acid detection reagent for detecting 1000 or more

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RESULT 1:
ABB70054
ID ABB:
XX ABB7054
AC ABB:
XX ABC ABBC
XX Dros
XX D
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher entaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB16737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                        Drosophila melanogaster
  WPI; 2001-656860/75
                                        Venter
                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                           23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                  27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                 pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                       Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB70054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB70054 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes from Drosophila
                                                                              (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 EIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFD----SCNVA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAFKFPDSMNVHFQCVIQVC----RYNCPEPKC-----GPGLPGGEYGLPQIGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDMLHAVTANFLGDNLQ------CWMQIQVGKGPWASEVSGIVKIGQTMTMVLAIKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEVSEITTA-----FQTQIVPMPVCRYEILDG-GPTGQPVQFAI-IGQPVYHKWTCDSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSANHNAAGYGAPTPSGSYVENTIIIQYDPYVQEVWDQARKLRCTWYDFYEKAVTFRPFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQCEKTHMRVNIEFDRPFYGMIFSKGFYSDPHCVHLKPG--TGHLSATFEIFLNSCGMT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-NKFDMLVRNCVAHDGKRAPIQLVDQNGCVVRPKIMSKFQKIKNF--GPSASVVSFAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTRSLN-----PRGIFVTTTVVISFHPLFVTKVDRAYRVQC----FYMEADKTVSAQ
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63; Conserv
                                      JC,
                                                                              CORP NY.
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                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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Pred. No. 4.1
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                                      Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126;
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                                                                                                               23-MAR-2001; 2001WO-US09231
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Query Match
Best Local S
Matches 63
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                                                                                                                                                                       Sequence
                                                                                                                                                                                                                            specification, but was obtained in electronic format directly from
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 36954; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
30 EIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFD----SCNVA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an isolated nucleic acid detection reagent uble of detecting 1000 or more genes from Drosophila. The invention
                                                        63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL14157
                                                                                                                                                                          611 AA;
                                                                                8.0%;
                                                           51;
                                                        Score 162.5; DB:
Pred. No. 4.1e-08,
1; Mismatches 120
                                                                                                                 DB 22;
                                                        Indels
                                                                                                              Length
                                                                                                                 611;
                                                        55;
                                                     Gaps
                                                                                                                                                                                                                                                          WIPO
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                                                           13;
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QAFKFPDSMNVHFQCVIQVC----RYNCPEPKC RTRSLN-----PRGIFVTTTVVISFHPLFVTKVDRAYRVQC----FYMEADKTVSAQ 133 --YKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAA E-NKFDMLVRNCVAHDGKRAPIQLVDQNGCVVRPKIMSKFQKIKNF--GPSASVVSFAYF TVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHV-----VDMLHAVTANFLGDNLQ---IEVSEITTA-----FQTQIVPMPVCRYEILDG-GPTGQPVQFAI-IGQPVYHKWTCDSE 185 SSANHNAAGYGAPTPSGSYVENTIIIQYDPYVQEVWDQARKLRCTWYDFYEKAVTFRPFQ QVQCEKTHMRVNIEFDRPFYGMIFSKGFYSDPHCVHLKPG--TGHLSATFEIFLNSCGMT 145 ----CWMQIQVGKGPWASEVSGIVKIGQTMTMVLAIKDD ---GPGLPGGEYGLPQIGA 359 292 239 257

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Drosophila melanogaster polypeptide SEQ ID NO 1803
pharmaceutical
                     Drosophila;
                                                                                                  26-MAR-2002
                                                                                                                                        ABB58337;
                                                                                                                                                                                ABB58337 standard; Protein; 758
                developmental biology; cell signalling;
                                                                                                (first entry)
                                                                                                                                                                                AA
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27-SEP-2001 WO200171042-A2 Drosophila melanogaster insecticide;

(PEKE ) PE CORP NY 23-MAR-2000; 11-JUL-2000; 2000US-191637P 2000US-0614150

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RESULT 13
ABB58185
ID ABB58
XX ABS8
XX ABS8
XX Z6-MA
DT 26-MA
XX Droso
XX Droso
XX Pharm
XX Pharm
XX Pharm
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Best Local :
                                                                                WO200171042-A2
                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                  pharmaceutical
                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                             ABB58185
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                                                                                                                                                                                                                                                                                                                                                                                                         ABB58185 standard;
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es from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTDGVELAIKSERQKRDVSHQAAGDENILLVQ----SIQITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAVVHSCFVDDGNGDTVEI--LNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYA-DRSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVART---RSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISD 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSQFD---AFKFPSSELVQFRALVTPCIPRC-EPVICDNDENGELKSLLSYGRRKRSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFYQCQISITIKEPNSECVR------PQCSEP------QGFGAVK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIFVRELVAMDGT-DSAEITLIDANGCPTDQYIMSAMQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIESTLSEEIIVDSPNVIMKITARDG----SDMKRIAEVGDPLALRF----EIVDANSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEITTAFQTQIV---PMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDT---F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVRQSAYGRYMN------DIVIQHHDMIVTSSDLGLAVSCQYDLTNKTVVNNVDLGVT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFD-----SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDCRSGEMITKIRTSKLFDGKYYAKGA--PKSCAVNVNN-----SLEFDLKMRYNDLEC
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                                                                                                                                                                                                       developmental biology;
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Pred. No. 1.3e-06;
0; Mismatches 114;
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                                                                                                                                                                                                       insecticide;
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at ftp.wipo.int/pub/published_pct_sequences.
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genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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11-JUL-2000;
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                       FGFSMFMGLSIALIAAVIITISFKFRP 383
                                                                                                                                                                                                                                                                                                      NVART---RSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEV---
                                                                                                                                                                                                                                                                                                                                         IECRSGEMITKIRTSKLFDGKVYAKGA--PKSCAVNVNN-----SLEFDFRMGYNDLEC
-----DDNILLMQSIQITDKFGFQP
                                                                                 -KKRSAEPENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSP
                                                                                                                                          QCQISITIKEPNSECVR------PQCSEPQGFGAVKTGGAAAKPAAAAQLRLL----
                                                                                                                                                                    VRELVAMDGS-DSAEITLIDANGCPTDQYIMGTIQ----
                                                                                                                                                                                               VHSCFVDDGNGDTVEI--LNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYA-DRSQLFY
                                                                                                                                                                                                                           GEIESSLSEEITIDSPNVIMKITSRDG---SDMKRMAEVGDPLALRFEI-VEPNSPYEIF
                                                                                                                                                                                                                                                      SEITTAFQTQIV---PMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAV
                                                                                                                                                                                                                                                                                    NVRQSAYGRYMN------DIVIQHHDMIVTSSDLGLAVSCQYDLTNKTVLNDVDLGVT
                                                                                                             QFD---AFKFPSSEVVQFRALVTPCIPRC-EPV-----ICDSEDGASGELKSLVSYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                      -GTDGAEFLISTRHR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21pp + Sequence Listing;
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Pred. No. 1.1e-05;
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Drosophila melanogaster polypeptide SEQ ID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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627
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                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 63; Conser
EKR 629
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                                                                                                                  ARTSFKIIDDDGCPTDPTIFPG--FTADGNALQSTYEAFRFTESYGVIFQCNVKY----
                                                                                                                                                                                                           QTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGN
                                                                                                                                                                                                                                        TQSVT--GVY-SNTVVLQHHSVVMTKADKIYKVKCTYDMSSKNITFGMMPIRDPEMIHIN
                                                                                                                                                                                                                                                                      TRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVS----AQIEVSEITTAF 143
                                                                                                                                                                                                                                                                                                   VHCKDTRIAVQVRTNKPFNGRIYALG--RSETCNIDVINSDAFR--LDLTMAGQDCN---
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                                                         ---CLGP-
                                                                                   NSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISD
                                                                                                                                                GDT-VEILNADGCALDKYLLNNLEYPTDLMAGQEAH-VYKYADRSQLFYQCQISITIKEP 261
                                                                                                                                                                             SSPEAPPP--RIRILD--TRQREVETVRIGDRLNFRIEIPEDT--PYGIFARSCVAMAKD
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                                                         -AVCEWNMDSFESLGRRRRRSIESNDTKSEDDMNISQEILVLDFGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and interactions -
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P--SSEVVQFRALVTPCMPSCEPV--QCEQEDTSGEFRS--
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                        ADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLL----K 298
                                                    VAMDGVDNSEITLIDSNGCPTDHFIMGPIYKGSVSGKMLLSNFD-
                                                                              CFVDDGNGDTVEILNADGCALD-------KYLLNNLEYPTDLMAGQEAHVYKY 242
                                                                                                          MPALSEEVIVESPNVIMRITSRDG---SDMMRSAEVGDPLALKFEIVDEQSPYEIFIREL 543
                                                                                                                                    TTAFQTQIV----PMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHS 196
                                                                                                                                                               NVRQSTA---
                                                                                                                                                                                        NVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEV---SEI 139
                                                                                                                                                                                                                      IECGGGDMLARIRTSKLFNGKVYAKG--SPKSCSVD-----VKSALDFELRMNYHDLEC 431
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPC of the printed the proteins are controlled to the printed and the proteins are controlled to the printed and the printed are controlled to the printed and the printed are controlled to the printed are controlled to the printed and the printed are controlled to the printed are controlled 
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                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                               EIECGPTSITINFNTRNAFEGHYYVKGLYDQEGC--RNDEGGRQVAGISLPFDSCNVART 87
PDLN--GQFYENTVVVQYDKDLLEVWDEAKRLRCEWFNDYEKTASKPPMVIADLDVIQLD 123
                                        RSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQC-FYMEADKTVS-----AQIEVSEIT 140
                                                                                         EVMCGKDHMDVHLTFSHPFEGIVSSKGQHSDPRCVYVPPSTGKTFFSFRISYSRCGT--K
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Pred. No. 0.00013;
3; Mismatches 110
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                                                                                                                                                              Local Similarity es 80; Conserv
                                                                                          EIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRN-DEG-GRQVAGISLPFDSCNVA--
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                                                                                                                                                                                                                                                                      699 AA;
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2000US-0614150
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Pred. No. 0.00066;
7; Mismatches 182;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10167-ABL30511), expressed DNA sequences (ABL01040-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                Disclosure;
                                                                                                                                                                       New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                     WPI; 2001-656860/75
N-PSDB; ABL12267.
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11-JUL-2000;
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                                                                                                                                SEQ ID NO 31284;
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2000US-0614150
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Best Local S
Matches 78
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                            -- NGQPVILAAVQNGICMSPFGFSMFMGLSIAL
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                                                         SSANKVYEISLAMFLQVQDIEGVNKNEVLQLEEKLRELKLA--NQRLARNSRGNFAMEQT
                                                                                      AAAKPAAAAQLRL-LKKRSAEPEN---IIDVRTDINTLEISDDNQALPVDLRHRALLQH-
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                                                                                                                                                                                                                                                                                                                                                      GSHKVHCSEDQMRVDIGLPDAESKDQSAPQIYLEGLKGYPDERCQPQIDGSLAVFRLSLS
                                                                                                                 FNTIDGDILSAKFKAFKFPDSSYVQFRATVNVCL----DKCLGTQCSNNQVGFGRRKREI
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19.8%;
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       New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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DB; ABL15537.
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Best Local
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      Venter JC,
                                 (PEKE ) PE CORP NY.
                                                           23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                               23-MAR-2001; 2001WO-US09231
                                                                                                                                                      WO200171042-A2
                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                                                        Drosophila;
                                                                                                                            27-SEP-2001
                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 32772
                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                            ABB68660 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                               322 STDPQC
                                                                                                                                                                                                                                                                                                                                                                                                                          268 --- PQC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 EIECGPTS---ITINFNTRNAFEGHVYVKGLYDQEGC---RNDEGGRQVAGISLPFDSCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSTYYNT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVKHSEQAWDINILQCYASDDMDFEARTTKRLQLSDKRGCSIKEKIFGEWRKFEAGSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVVDMLEVISVDTPSGPVECWMEIGTGTPPNVKPIQGTLTLGTDI-----TFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVSEITTAFQTQIVPMPV-CRYEILDGGPTG-QPVQFAI-IGQPVYHKWTCDSETVDTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARTRSLNPRGIEVTTTVVISFHPLFVTKVDR-----AYRVQCFY-MEADKTVSAQI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVKCDQGSGMMVEVEFS--EDFEGVIYSQGYFSDPKCNYVKGDRSGRSFT-FTVPYDGC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
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                                                                                                                                                                                                                    developmental biology;
      Adams M,
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                                                                                                                                                                                                                                                                        (first entry)
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      DWD,
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Pred. No. 0.13;
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                                                                                                                                                                                                                    insecticide;
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Protein
             Region
                                                                                            Xenopus
                                                                                                                     Amidation; PHL.
                                                                                                                                             AE-III (peptidylhydroxyglycine
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                                                                                                                                                                                                     AAR20112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 32772; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                             212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 CGPTSITINFNTRNAFEGHYYVKGLYDQEGCRNDEGGRQV-----AGISLPFDSCNVART 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                         ADGCALDKYL---LNNLEYPTDLMAGQEAHYYKYADRSQLFYQCQISITIKEPN-SECV-
                                                                                                                                                                                                                                                                                             SSWQRRRRQADQP
                                                                                                                                                                                                                                                                                                                                                                                                                              ----RPQCSEP
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DB; ABL12763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AFQTQIV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEMTQEYQRTFISALVVIQNNPNVQTQGDRLIKVGCIQSNATTSLGVSVRDSSVDSSEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSLNP--RGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITT----
                                                                                            laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                         (first entry)
           /label= AE-III
/note= "including
383..935
/*tag=
                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                              627
                                                                                                                                                                                                                             Protein;
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Pred. No. 0.3;
55; Mismatches
                                                                                                                                            N-C lyase precursor).
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                          PAM
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DB 120;

22;

Indels Length

87;

Gaps

11;

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448

168

141

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NENFYLLID

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614

266 554

and PHL

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Best Local
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01-JUN-1990;
10-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence was deduced from a cDNA insert from pAE-III-202-4 (FERM BP-3172). The vector serves as a source for a DNA fragment encoding PHL for the construction of an expression vector for the prepn. of recombinant PHL. The protein may be truncated to comprise only residues 383-706 or 383-713. The PHL catalyses the reaction: R-GlyOH -> R-NH2. It can be used to produce peptides wit amidated C-termini, e.g. calcitonin, growth hormone, LH-RH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel DNA encoding peptidyl hydroxy:glycine N-C lyase used to prepare PHL which can be used in the amidation peptide(s) e.g. human calcitonin.
             ABB71814
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Kawahara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                 757
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                                                                                                                                                                                                                                                                                                                                                                                                                      33 CGPTSITINFNTRNAFEGHYYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNP
                                                                                                  CMSPFGFSMFMGLSIALI-AAVIITISFKFR 382
                                                                                                                                                                                                                                    SAPVQGEMLNESNGD------ILDTEIPARKNEDMPHDIAAADDGTVYVGDAHANA
                                                                                                                                                                                                                                                                                                                                                                     RGIFV------TTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVS
                                                                                                                                                                                                                                                                                                                                                                                                CQPTDVAVDPITGNFFVADGY------
                                                                           QESSAGVSFVLITLLIIPIAVLIAIAIFIR 847
                                                                                                                                                                                 VWKFSPSKAEHRSVKKAGIEVEEITETEIFETHIRSRPKTNESVEKQTQEKQQK--QKNS
                                                                                                                                                                                                        FYQCQIS----ITIKEPN---SECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRS
                                                                                                                                                                                                                                                            CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVYKYADRSQL
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                                                                                                                              AGVSTQEKQNVVQEINAGVPTQEKQNVVQESSAGVSTQEKQSVVQESSAGVSTQEKQSVV
                                                                                                                                                     A-----EPENII-DVRTDINTLE---ISDDNQALPVDLRHRALLQHNGQPVILAAVQNGI 352
                                                                                                                                                                                                                                                                                       -QIKHQEFGREVFAVSYAP-----GG-----VLYAVNGKPYY------GY
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            standard;
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90JP-0141678.
90JP-0210535.
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            Protein;
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            227
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Pred. No. 0.47
57; Mismatches
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Best Local Similarity
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ChabS7737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                         27-JUN-1990
                                                 AAP94856;
                                                                         AAP94856 standard;
                                                                                                                                                                                                                                                                                                                                                Sequence
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genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB71814;
                                                                                                                                        158
                                                                                                                                                                                           104
                                                                                                                                                                 131 SAQIEV---SEIT 140
                                                                                                                                                                                                                     76
                                                                                                                                                                                                                                             46
                                                                                                                                                                                                                                                                 22 DNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGC-----RNDEGGRQVAGI
                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-656860/75.
                                                                                                                                        QARDRVATGSKIT
                                                                                                                                                                                           NFQLDQCQTIRD-----GDLYTNIVVIQNDPELITPGDSAFSLECDFRQPRNLDVEASM
                                                                                                                                                                                                                  SLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFY----MEADKTV 130
                                                                                                                                                                                                                                             DQGIQ-KVNLKCGADSMNVVLETEKPFMGVMYTRGSFYKQSAPCFMKPSSSQGSRTME-M
                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL15917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                  227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-191637P.
2000US-0614150.
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                  A,
                                                                                                                                        170
                                                                         protein;
                                                                                                                                                                                                                                                                                                           4.8%;
22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                           Score 97; DB 2
Pred. No. 0.1;
29; Mismatches
                                                                           693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers
                                                                           A
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                                                                                                                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000 or more and cell-cell
                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                           157
                                                                                                                                                                                                                                             103
                                                                                                                                                                                                                                                                    75
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Expression plasmid pUCPlCI799

BglII gene product.

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RESULT 24
AAP94854
ID AAP94
XX AAP94
AC AAP94
XX 27-JU
DT 27-JU
DE C-ter
XX Alpha
XX Alpha
XX Synth
XX Synth
XX EP299
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                 Synthetic
                                                      alpha-amidating;
                                                                           C-terminal prepro-C-terminal alpha-amidating
                                                                                                    27-JUN-1990
                                                                                                                           AAP94854;
                                                                                                                                               AAP94854 standard; protein; 875
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encodes a derivative of the mature C-terminal alpha-amidating enzyme from plasmid pXA799.

The plasmid was screened from an E.coli library using plasmid pXA457 to screen a larger library.

Although pXA799 is similar to pXA457 at the N-terminus, it has an argot hydrophobic elements suggesting a membrane function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohsuye K, Kitano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1987;
05-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-amidating; pAX799; alpha amide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant C terminal alpha amidating enzymes of Xenopus laevis - and their precursors deoxyribonucleic acid encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP299790-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1988;
                                                                                                                                                                                                       621
                                                                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                 522
                                                                                                                                                                                                                                                                                                                                            491
                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                33 CGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNP 92
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          also AAN93060.
                                                                                                                                                                                                       -----MLNFSNGD------ILDTFIPARKNFEMPHDIAAGDDGTVY
                                                                                                                                                                                                                            CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVY
                                                                                                                                                                                                                                                                        AQIEVSEI-TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTF 190
                                                                                                                                                                                                                                                                                             NGMFIMQWGEETSSNLPRPGQFRIPHSLTMISDQGQLCVADRENG-RIQCFHAKTGEFVK
                                                                                                                                                                                                                                                                                                                       RGIFV----
                                                                                                                                                                                                                                                                                                                                           CQPTDVAVDPITGNFFVADGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1989-017279/03.
                                                                                                                                                                                                                                                    -QIKHQEFGREVFAVSYAP--
                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                     693 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87JP-0177184
87JP-0306867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88EP-0306508
                                                      pAx799; alpha amide;
                                                                                                                                                                                                                                                                                                                                                                                 4.7%; pre
21.6%; pre
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                Score 94.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s
                                                                                                                                                                                                                                                 -----GG-----VLYAVNGKPYYG----DSTPVQGF
                                                                                                                                                                                                                                                                                                                   TTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVS 131
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                               A
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                                                       ds
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                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                           -----CN-SRIMQFSP
                                                                            enzyme
                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~
                                                                            of.
                                                                           pxA799
                                                                                                                                                                                                                                                                                                                                                                                                             693;
                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                      655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has an area
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                              580
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RESULT 25
AAR73053
ID AAR73
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                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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Best Local S
Matches 50
                                                                       Key
Peptide
07-SEP-1994;
                      26-APR-1995
                                                                                                        Not specified
                                                                                                                                                            Peptidyl C-terminal alpha-amidating
                                                                                                                                                                                 06-NOV-1995
                                                                                                                                                                                                       AAR73053;
                                                                                                                                                                                                                           AAR73053 standard; Protein;
                                         EP649900-A.
                                                                                                                             trichostatin;
                                                                                                                                       Peptidyl C-terminal alpha-amidating enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to screen a larger library.
Although the gene product is similar to that of pxa
N-terminus, it has an area of hydrophobic elements
function. See also AAN93060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pxA799 contains a sequence derived from Xenopus laevis The plasmid was screened from an E.coli library using plasmid p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant C terminal alpha amidating enzymes of Xenopus laevis and their precursors deoxyribonucleic acid encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-017279/03.
N-PSDB; AAN90791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1987;
05-DEC-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-1989
                                                                                                                                                                                                                                                                                660
                                                                                                                                                                                                                                                                                                   191 CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVY 240
                                                                                                                                                                                                                                                                                                                         620
                                                                                                                                                                                                                                                                                                                                              132
                                                                                                                                                                                                                                                                                                                                                                 561 NGMFIMQWGEETSSNLPRPGQFRIPHSLTMISDQGQLCVADRENG-RIQCFHAKTGEFVK 619
                                                                                                                                                                                                                                                                                                                                                                                                             93
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                                                                                                                                                                                                                                                                                                                                          AQIEVSEI-TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                               CGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNP 92
                                                                                                                                                                                                                                                                                -----MLNFSNGD-----
                                                                                                                                                                                                                                                                                                                                                                                       RGIFV----
                                                                                                                                                                                                                                                                                                                         -QIKHQEFGREVFAVSYAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 4.7%;
l similarity 21.6%;
50; Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               875 AA;
                                                                                                                                                                                (first entry)
                                                                                                                              CHO.
94EP-0306587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87JP-0177184.
87JP-0306867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88EP-0306508
                                                            /label= Sig_peptide
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka
                                                                                                                                                                                                                                                                                ----ILDTFIPARKNFEMPHDIAAGDDGTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                            875
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94.5; D
Pred. No. 1.6;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                                                         ----GG-----VLYAVNGKPYYG----DSTPVQGF
                                                                                                                                                                                                                                                                                                                                                                                      -TTTVVISEHPLEVTKVDRAYRVQCEYMEADKTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuo
                                                                                                                                                            enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                       ΑE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                        cell culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pxA457 at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 875;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             suggesting a
                                                                                                                                                                                                                                                                                694
                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PXA457
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane
                                                                                                                                                                                                                                                                                                                          659
                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                             560
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RESULT 26
ABB63130
ID ABB63
XX ABB63
AC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3mu-1S cells (i.e. CHO cells expressing a peptidyl C-terminal alpha-amidase enzyme (AE)) were suspended in F-12 medium to which aliquots of trichostatin were added. Cells were cultured for 3 days at 37 deg and then assayed for AE. Without trichostatin, AE productivity was 708 U/ml. At 10, 50, 100 and 200 nM trichostatin, AE productivities were respectively 866, 1897, 1894 and 3359 U/ml.
                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 16182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB63130 standard; Protein; 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 10-15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing protein prodn. from a trichostatin to the medium, injurious to host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-156754/21.
N-PSDB; AAQ87970.
                                                                                23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                23-MAR-2001;
                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                         WO200171042-A2
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                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FURU/) FURUKAWA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 NGMFIMQWGEQTSSNLPRPGQFRIPHSLTMISDQGQLCVADRENG-RIQCFHAKTGEFVK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQIEVSEI-TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQPTDVAVDPITGNFFVADGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QIKHQEFGREVFAVSYAP-----GG-----VLYAVNGKPYYG----DSTPVQGF 659
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                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling;
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                                                                                2000US-191637P.
2000US-0614150.
                                                                                                                                                                2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 27
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Was obtained in electronic format directl
                                                                                                                                                                                                                                                                                         Cyanophycin; synthase; enzyme; thermostable; feed supplement; protection; paper; textile; pigment; paint; ceramic; washing;
09-AUG-2000; 2000DE-1038775
                                                    27-JUL-2001; 2001WO-EP08690.
                                                                                                         14-FEB-2002
                                                                                                                                                             WO200212459-A2
                                                                                                                                                                                                               Synechococcus elongatus
                                                                                                                                                                                                                                                                      water treatment.
                                                                                                                                                                                                                                                                                                                                                                          Synechococcus cyanophycin synthetase SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB08760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SEITTAFQTQ-----IVPMP-----VCRYEILDGGPTGQPVQFAIIGQPVYHKW 180
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Best Local (
              pharmaceutical.
                         Drosophila; developmental biology;
                                                     Drosophila melanogaster polypeptide SEQ
                                                                                  26-MAR-2002
                                                                                                                ABB64427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a thermostable cyanophycin synthetase (I) with temperature optimum 35-550C. (I) is used for preparation of cyanophycin or its downstream products, especially poly(aspartic acid) and arginine. Cyanophycin and its products are useful as feed supplements, in plant protection and in the paper, textile, pigment, paint, ceramics, building materials and washing composition industries, also for (waste) water treatment. (I) has better heat stability than known enzymes, so allows production of cyanophycin at temperatures over 350C (the usual maximum), resulting in greater flexibility in process control, improved yield and reduced risk of contamination.
                                                                                                                                           ABB64427 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 23-25; 29pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cyanophycin synthase, downstream products, e.g. also related nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                        VDLRHRALLQHNGQPVILAA-----VQNGICMSPFGFSMFMGLSIALIAAVIIT
                                                                                                                                                                                                                                                                   --ADDPLVAAMARQVKAQVAYFSMDPHNPI-IRQHIQQGGLAAVYENGYLSILKGDWTLR
                                                                                                                                                                                                                                                                                               GAAAKPAAAAQLRLLKKR----SAEPENIIDVRTDINT------LEISDDNQALP
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                                                                                                                                                                                                                                                                                                                                                    D----RSQL-FYQCQISI-------TIKE-PNSECVRPQCSEPQGFGAVKTG
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             red. No. 3.2;
Mismatches
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                       cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EICYLRATANLSTGGI 398
                                                      ID NO 20073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                              2005
                                                                                                                                                                                                                                                                                     1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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11-JUL-2000;
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                            LEISDDN 323
                                                       QKRNENSECIISYGNSPKSFYVQMKHNSADLDLIVKTLQSLKKEKL--KKLIDPTTNSNG
                                                                                                                                         FVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISIT
                                                                                                                                                                                                EILDGGPT-----GQPVQFAIIGQPVYHKWTCDSE------TVDTFCAVVHSC
                                                                                                                                                                                                                            MDIICEKLNGSKLQPKTEKAAVDDMCVVQFADDLEFYRSRILEVLEDDQYKVI-----
                                                                                  IK-EPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINT
                                                                                                                                                                                                                                                                                                             RQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEAD--
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                                                                                                                                                                       -LIDYGNTTVVDKLYELPQEFTLI-KPVAE--ICSMEPSAIFEKNKALTLTTFDALLDSC
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Query Match
Best Local Similarity
                                                                                                                                                                        The present sequence is the protein encoded by Trim3 construct. pIL2Trim3 variant was constructed by removing the human IL2 residues from solCD39 fusion construct. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, intracardiac thrombosis, peripheral artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-1998;
06-NOV-1998;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DT; peripheral artery thrombosis; transient ischaemic attack; thrombus formation; ps; pulmonary embolism; transient ischaemic attack; thrombus formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides -
                                                                                                         thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Soluble (DB) is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood
                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-339518/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soluble CD39;
                                                                                              vessels or
                                                                                                                                                                                                                                                                                                                                                                                                     Example 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maliszewski CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-1999;
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                                                                                              stroke.
                                                                                                                                                                                                                                                                                                                                                                                                Page 113-114; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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98US-0107466.
99US-0149010.
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RES 1
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                    Length 474;
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06-NOV-1998;
13-AUG-1999;
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New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury -
                                                                                                                                                                         Maliszewski CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
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99US-0149010.
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36..474
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                                                                                                                                                                         Gayle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·GDT - - VEILNADGCALDKYLLNNLE - - - - - YPTD - - - - - LMAGQEAH
                                                                                                                                                                         RВ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cleavage site of leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474
                                                                                                                                                                         Price
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                                                                                                                                                                         ΥĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD39
                                                                                                                                                                         Gimpel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin 2 (hIL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ETFGALDLGGASTQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 31
AAY70901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the fusion protein construct, pIL2LTrim3. This construct comprises of the leader peptide from human interleukin 2 (HIL2) and soluble CD39 (solCD39) protein region, having apyrase activity. CC soluble CD39 is constructed by removing the N- and C-terminal CC transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse CC ADP-induced platelet activation and recruitment, including platelet CC aggregation. Soluble CD39 polypeptides are useful for inhibiting CC angiogenesis. It is useful for the treatment of unstable angina, stroke, CC myocardial infarction, coronary artery disease or injury, embolism, CC atherosclerosis, peripheral vascular occlusion, preeclampsia, platelet-cc associated ischaemic disorders including lung, coronary and cerebral cischaemia, thrombosic disorders including coronary, peripheral and CC cerebral artery thrombosis, intracardiac and venous thrombosis, (PE) and CC coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and CC thrombus formation or reformation, occlusion, reocclusion, stenosis or restormation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                             Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombotytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis;
                                             peripheral artery thrombosis; coagulopathy; deep venous thrombosis; DW; PE; pulmonary embolism; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; pIL2Trim4 variant.
Synthetic
                                                                                                                                                                                                                                                                                                  Protein encoded by Trim 4 construct.
                                                                                                                                                                                                                                                                                                                                            17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                   AAY70901;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY70901 standard; Protein; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restenosis of blood vessels or stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 VDRAYRVQCFYME-ADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 TEVPQNQTIE----SPDNALQFR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 IGOPVYHKWTCDSETVDTFCAVVH------SCFVDDGN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAQLRLLKKRSAEPENIIDVR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYGWITINYLLGKFSQKTRWF-----SIVPYETNNQ------ETFGALDLGGASTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VY------KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------YPTD-----LMAGQEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YKWPAEKEN-DT--GVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDRMQLLSCIALSLALVINSASTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 113-114; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 AA;
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87.5; D
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                  disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
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                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein encoded by Trim4 construct. pIL2Trim4 coration of activation of 12 mino acids from the N-terminus of mature fusion construct. Fusion of 12 mino acids from the N-terminus of mature chaman IL2 to the solcD39 coding region results in high levels of both C expression and activity in the supernatants of transfected cells. SolcD39 is used in the treatment of unstable angina, myocardial infarction, CC stroke, coronary artery disease or injury, atherosclerosis, peripheral CC vascular occlusion, precclampsia, embolism, platelet-associated ischaemic C disorder including lung ischaemia, coronary ischaemia and cerebral CC disorder including lung ischaemia, coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischaemic attack. Teformation, occlusion, reocclusion, stenosis or restenosis of blood
                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD2 polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-1998;
06-NOV-1998;
13-AUG-1999;
                                                                174
                                                                                                                                   114
220 FVPQNQTIE----SPDNALQFR 237
                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 11; Page 114-116; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                           173 GQPVYHKWTCDSETVDTFCAVVH------SCFVDDGN-----
                                                                                                                                                                                                                                                                                        113 VDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAII 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maliszewski CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX (CORR ) CORNELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200023094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                          5 IDRMQLLSCIALSTALVTNSSTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYI---
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                          PRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGA
                              AAAQLRLLKKRSAEPENIIDVR 311
                                                                YGWITINYLLGKFSQKTRWF----SIVPYETNNQ-
                                                                                                                                                                                           ----YKWPAEKEN-DT--GVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVI 113
                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                               stroke.
                                                                                                                                                                                                                                                                                                                                                                                                473 AA;
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                           KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0149010
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98US-0107466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US23641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP
                                                                                                                                                              -GDT--VEILNADGCALDKYLLNNLE-----YPTD-----LMAGQEAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gayle RB, Marcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 26..27 35..473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-
                                                                                                                                                                                                                                                                                                                                             4.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Soluble portion
                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                            Score 87; DB:
Pred. No. 4;
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of CD39"
                                                                                                                                                                                                                                                                                                                                                           21; Length 473;
                                                                                                                                                                                                                                                                                                                          77;
                                                             ETFGALDLGGASTQVT
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                                                          Gaps
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CD39

219

61 203

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RESULT 32
AAY70924
ID AAY70
at relevant concentrations and the addition in cluding platelet apprehenced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, stroke, myocardial infarction, coronary artery disease or injury, embolism, atherosclerosis, peripheral vascular occlusion, preclampsia, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombosis or formation or reformation, occlusion, reocclusion, stenosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-1998;
06-NOV-1998;
13-AUG-1999;
                                                                                                                                                                                                                         The present sequence is the fusion protein construct, pILZLTrim4. This construct comprises of the leader peptide from human interleukin 2 (hIL2) and soluble CD39 (solCD39) protein region, having apyrase activity. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DV; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unstable angina; myocardial infarction; stroke; atherosclerosis; peripheral vascular occlusion; platelet-associated ischaemic disorder; thrombot
                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 114-116; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY70924 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maliszewski CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200023459-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble CD39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-2000
              restenosis
             O.
                                                                                                                                                                                                                                                                                                                                                                                          stroke, coronary artery disease or injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
             blood vessels or stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           solCD39; human; apyrase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD39 fusion protein construct, pIL2LTrim4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0104585.
98US-0107466.
99US-0149010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Leader_peptide
/note= "Derived from human interleukin 2 (hIL2)"
26..27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Cleavage site of leader sequence"
35..473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gayle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Price VL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preeclampsia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coronary artery disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embolism;
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RESULT 33
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Best Local
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                   28-OCT-1994;
                                       11-MAY-1995
                                                           WO9512661-A
                                                                                          Misc-difference
                                                                                                                     Misc-difference 1450..1460
/label= misc
                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                           Aspergillus
                                                                                                                                                                                                                                                                                                                                               hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                          Triol polyketide synthase; TPKS; HMG-CoA reductase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                              Aspergillus terreus triol polyketide synthase
                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR74171;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR74171 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 VDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAII 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 PRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 FVPQNQTIE----SPDNALQFR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 AAAQLRLLKKRSAEPENIIDVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 IDRMQLLSCIALSLALVTNSSTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGWITINYLLGKFSQKTRWF-----SIVPYETNNQ------ETFGALDLGGASTQVT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YKWPAEKEN-DT--GVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQPVYHKWTCDSETVDTFCAVVH-----SCFVDDGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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                   94WO-US12423
                                                                                                                                                  282..288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPA 289
                                                                                                              1603..1612
                                                                                          2521..2535
                                                                                                                                                                          2498
                                                                                                                                                                                           /label= enoyl reductase motif
2164..2169
                                                                                                                                                                                                              1446..1450
/label= methyl transferase motif
1932..1937
                                                                              /label=
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                   /label= keto-acyl synthase motif
                                                                                                  'label= misc
                                                                                                                                          'label- misc
                                                                                                                                                                                .abel= keto
                                                                                                                                                            abel acyl carrier protein motif
                                                                                                                                                                                                                                            abel=
                                                                                                                                                                                                                                                                abel- acetyl/malonyl transferase motif
                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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19.58;
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                                                                                                                                                                                                                                            dehydratase motif
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          3038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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26-JUN-2001

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RESULT 34
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Best Local :
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             AAB94352;
                                      AAB94352 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The full-length TPKS-encoding DNA in plasmid pLOA was designated pPFKS100. Splicing of the introns from the DNA sequence and translation of the 9114 mt ORF results in a protein of 3038 AAS (AAR74171) with a mol. wt. of 269,090 daltons. Inspection of the TPKS AA sequence for active site residues and motifs known to be associated with polyketide synthases and fatty acid synthase (FAS) activities resulted in the identification of candidates for expected sites (see FT). Except for the presence of a methyl transferase, not present in FAS, the succession of activities on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1175 VAFQTVIGA--YSSP-----GDRRLRCLYVPTHVDRITLVPSLCLATAESGCEKVAFNT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel DNA encoding triol poly-ketide synthase - used to isolate and identify homologues of triol poly-ketide synthase, and in the treat of hyper-cholesterolaemia
                                                                                                                                                                                                                                                                                                                     202
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Reeves CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-193816/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 RNAFEGHVYVKG---LYDQEGCRNDEGGRQVAGISL-PFDSCNVARTRSLNPRGIF--VT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 IAFCTTLIALSYSIPVDNGVEGEPEIEC--GPTSI-----TINFNT
                                                                                                        KTMAHARSLLKPGGQMVILEITHKEHTRLGFIFGLFADWWAGVDDGRCTEPF 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTYDKGDYLSGDIVVFDAE----QTTLFQVENITFKPFSPPDASTDHAMFARWSWGPLT
                                                                                                                                        VDLRH-RALLQHNGQPVIL--
                                                                                                                                                                 STGFFEQAREQFAPFEDRMVFEPLDIRRSPAEQGFEP-HAYDLIIASNVLHATPD---
                                                                                                                                                                                            ------RLLKKRSAEPENIIDVRTDINTLEISDDNQALP
                                                                                                                                                                                                                                                                                   RVGQHLLPTVRSNGNPFDLLDHDG-LLTEFYTNTLSFGPALHYARELVA-QIAHRYQSMD
                                                                                                                                                                                                                                                                                                                                          E----QVLASAKEGR-------HLWYDPGWENDTEAQIEHLCTANSYHPHVRLVQ
                                                                                                                                                                                                                                                                                                                                                                                                  PDSLLDNPEYWATAQDKEAIPIIERIVYFYI---RSFLSQLTLEERQQAAFHLQKQIEWL
                                                                                                                                                                                                                                                       RSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQL------
                                                                                                                                                                                                                                                                                                            PYCRYEILDGGPTGQPYQFAIIGQPYYHKWTCDSETVDTFCAVVHSCFYDD------
                                                                                                                                                                                                                                                                                                                                                                                                                             TTVVISFHPLFVTKVDR-----AYRVQCFYMEADKTVSAQIEVSEITTA---FQTQIVPM 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein is the same as that observed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davis CR,
Vinci VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ß
                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%;
19.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 87; DB
Pred. No. 77;
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                                                                                                                                                                                                                          GAG---TGGATKYVLATPQLGFNSYTYTDI
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                                                                                                                                      --- AAVQNGICMSPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary Strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC complementary to a complementary for sequence complementary to a complementary for sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers sets can be used in antisense therapy and complementary full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the particularly without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13637 to AAH13638 and complementary and a complementary and a complementary and a complementary and a complementary and complementary in the complementary and complementary full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13639 and A
                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 14870;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
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                                                                                             310 --DGKSLLSGLATGESGWSQHRQRRLQDHGKERKELFSTTT-----
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QCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTG---QPVQ-FAIIGQP
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                                                                                                                                                                                                                        VGFLSSLLPQSKKSPSRLSPAQGPPQ----PQSSA----KKESFGGQ-GTKGKDPTSGAK 309
                                                                                                                                                                                                                                                                                        IAFCTTLIALSYSIPVD-NGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCR 64
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84; Conservative
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; 99JP-0300253.
; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                               4.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                           Score 86.5; DB
Pred. No. 7.3;
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO:14870
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A, Nagai F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                             DВ
                                                                                                                                                                                                                                                                                                                                                              153;
                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Otsuki
                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             636;
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                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 35
AAM40070

AC AAM40

XX AAM40

XX AAM40

XX AAM40

DT 22-0X

XX Huma

XX Huma

XX Huma

XX AAM5

XX Huma

XX AAL2

XX AAM5

PN WO2

XX AAM5

PN WO2

XX BAN5

PN WO2

XX AAM5

PN WO2

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PN 1:

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                     in gene therapy. A co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic; chemotinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM40070
                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153312-A1
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                                                                                                                                                               Example
                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia.
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                                                                                                                                                                                                                                                                                                                                                Y, LY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVKTGGAAAKPAAAAQLRL------LKKRSAEPENII--DVRTDINTLEISDDNQALPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLLSLEWATKRDRLLLLGSGVGTVRLYDTEAKKNLCEININDNMP--RILSLACS-PNGA
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                                                                                                                                                                                                                                                                                2001-442253/47.
)B; AAI59226.
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د.
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                                                                                                                                                                                                                                                                                                                                           Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 747 AA
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                                                                                                                                                               SEQ
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2000US-0693036.
2000US-0727344.
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2000US-0620312.
2000US-0653450.
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  peripheral
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Wehrman T,
Goodrich F
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                                                                                                                                                               3215;
                                                                                                                                                           10078pp; English.
  nervous
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                                                                                                                                                                                                                                                                                                                                                                 Chen R,
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injuries,
                                                                                                                                                                                                                                                                                                                                                                   Xue
                                                                                                                                                                                                                                                                                                                                           Ma Y,
Xue AJ,
ac RT;
                                                                                                                                                                                                                                                                                                                                                                   Qian XB,
Yang Y,
peripheral
                                                                                                                                                                                                                                  for
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                                                                                                                                                                                                                             treating
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                                                                                                                                                                                                                                                                                                                                                                   Zhang
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                                                                                                                                                                                                                                                                                                                                                                     Ģ
                                                                                                                                                                                                                                                                                                                                                                                        Wang
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and
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RESULT 36
AAB93124
ID AAB93124
ID AAB93
XX AB93
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX Homo
XX EP107
XX EP107
XX 29-JU
PR 27-AU
PR 27-AU
PR 11-JZ
PR 09-JU
XX OHEL1
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                                       29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.N.S
                            09-JUN-2000;
                                                                                                           28-JUL-2000;
                                                                                                                                    07-FEB-2001
                                                                                                                                                               EP1074617-A2
                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                         26-JUN-2001
                                                                                                                                                                                                                                                                                                   AAB93124;
                                                                                                                                                                                                                                                                                                                            AAB93124 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                NC--
                                                                                                                                                                                                                                                                                                                                                                                                                        DLRHRALLQHNGQPVILAAVQNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAVKTGGAAAKPAAAAQLRL-----LKKRSAEPENII--DVRTDINTLEISDDNQALPV 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QC----AEKKPEASGPEAEPCPELHTEPVE-PLTRAS--SAGPEGGGVRPEQPFIVLGQE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDEGGRQVAGISLPFDSCNVARTRSLNPRG-----IFVTTTVVISFHPLFVTKVDRAYRV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTG---QPVQ-FAIIGQP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DGKSLLSGLATGESGWSQHRQRRLQDHGKERKELFSTTT
                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders.
                                                                                                                                                                                                                   primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 21.9
84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                -TAFNHNGNLLVTGAADGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    -CSAAAPSLTSQVDFSAPDIGSKGMNQVPGRLLLWDTKTMKQQLQFSLDPEPIAI
                         99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                            2000EP-0116126
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                   detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·EHHSSIMH-CRV-DCSGRRVASLDVDGVIKVWSFNPIMQTKASSISKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              data
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                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                              IJ
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Pred. No. 9.4;
54; Mismatches
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                                                                                                                                                                                                                                              NO:12006
                                                                                                                                                                                                                                                                                                                                                                                                586
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the moreous transfer of the process to an acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 12006; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded
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                                                                                                                                                                                                                                   403
                                                                                                                                                                                                                                                                    176 VYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADG-------CALDKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 VGFLSSLLPQSKKSPSRLSPAQGPPQ----PQSSA----KKESFGGQ-GTKGRDPTSGAK
                                                                                                                                                                                                                                                                                                                                                                                                                               65 NDEGGRQVAGISLPFDSCNVARTRSLNPRG----IFVTTTVVISFHPLFVTKVDRAYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 IAFCTTLIALSYSIPVD-NGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T,
                                  DLRHRALLQHNGQPVILAAVQNGI
                                                                                                                                                                                         LLNNLEYPTD----LMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGF
NC - - - TAFNHNGNLLVTGAADGVI
                                                                                                           GAVKTGGAAAKPAAAAQLRL-----LKKRSAEPENII--DVRTDINTLEISDDNQALPV
                                                                                                                                                  PLLSLEWATKRDRLLLLGSGVGTVRLYDTEAKKNLCEININDNMP--RILSLACS-PNGA
                                                                                                                                                                                                                                                                                                         QC----AEKKPEASGPEAEPCPELHTEPVE-PLTRAS--SAGPEGGGVRPEQPFIVLGQE
                                                                                                                                                                                                                                                                                                                                   QCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTG---QPVQ-FAIIGQP
                                                                                                                                                                                                                                                                                                                                                                                          --- DGKSLLSGLATGESGWSQHRQRRLQDHGKERKELFSTTT----
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, Sugiyama T, Wakamatsu
                                                                       ---CSAAAPSLTSQVDFSAPDIGSKGMNQVPGRLLLWDTKTMKQQLQFSLDPEPIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                               -EHHSSIMH-CRV-DCSGRRVASLDVDGVIKVWSFNPIMQTKASSISKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86.5;
Pred. No. 9
                                    352
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A, Nagai K,
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he detection
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RESULT 37 ABP38294

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                                                                                                                                                                                                                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid encoding a Staphylococcus polypeptide, useful for diagnosing and treating bacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID 3139; 267pp; English.
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08-NOV-1997;
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318
                         343
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                                                                                                                                                                                                                                                              32 ECGPTSITINFNTRNAFEG--HVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRS
                                                                                                                                                                                                                                                                                                       Local
EISDDNQALPVDLRHRALLQHNG
                         DNEDTVLCA--DLIAPEGYGEIIGGSERIN----
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                                                                             AIEFLKKEG---
                                                                                                      TVETLNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRSQLF--YQCQISITIKEPNS
                                                                                                                                                       VPMPV--CRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGD
                                                                                                                               VQSVLNHCQLELK-----
                                                                                                                                                                                                          LNPRGIFVTTTVVISFHPLFVTKVDRAYR--VQCFYMEADKTVSAQIEVSEITTAFQTQI 147
                                                                                                                                                                                                                                    ENGFTKIDPPILTASAPEGTSELFHTKYFDEDAFLSQSG-----QLYMEAAAMAHGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-381255/41
DB; ABN90839.
                                                                                                                                                                                                                                                                                                                                                                       web
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                             438 AA;
                                                  -CVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTL
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97US-064964P
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gene therapy
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                                                                                                                                                                                  -VFSFGPTFRAEKSKTRRHLIEFWMIEPEMAFTNHAESLEIQEQYVSHI
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19.2%;
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                                                                             - FDDIEWGEDFGAPHETAIANHYDLPVFITNYPTKIKPFYMQPNP
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                                                                                                                                                                                                                                                                                         49;
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Pred. No. 5.1;
49; Mismatches
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                                                                                                                               -----ALDRDT--TKLEKVATPFPRISYDD
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                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                         127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coccus epidermidis bacterial infections
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                                                                                                                                                                                                                                                                                         85;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody reactive with part of desmosomal cadherin - exposed on surface of epithelial or carcinoma cells, not bound to desmosom useful for diagnosis and treatment of carcinoma micrometastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-146518/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW13009
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                                                                                                              DRAYRVQCFYMEAD---KTVSAQ--IEVSEITTAFQTQIVPM-PVCR-----YEILD
                                                                                                                                                                                                                                                                                                                                                LSYSIPVDNGVEGEPEI -- ECGPTSITINFNTRNAFEG-----HVYVKGLYDQEGCR 64
GGPTGQPVQFAIIGQP--VYHKW 180
                                                                                                                                                                                                                               NDEGGRQVAGISLPFDSCN----VARTRSLNPRGIF-----VTTTVVISFHPLFVTKV--
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                                                                                                                                                                      SSKG--QIIGNFQAFDEDTGLPAHARYVKLEDRDNWISVDSVTSEIKLAKLPDFESRYVQ
                                                     NGTYTVKIVAISEDYPRKTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLD
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560 AA;
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Pred. No. 7.6;
Pred. Mismatches
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RESULT 39
AAM39436
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                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity. Prager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                               Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance; peripheral nervous system; cRS; peripheral nervous system; cRS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; amyotrophic thrombolytic; drug screening; arthritis; inflammation; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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Sequence
                                     C.N.S disorders.
Note: The sequen
                                                                                                                                                                                                                                              Example 4; SEQ ID NO 2581; 10078pp; English.
                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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09-JUL-2000;
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Wehrman T,
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Zhang :
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Query Match Best Local Similarity

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Score Pred.

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3.5; 17;

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22;

Length

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RESULT 40
AAU78853
ID AAU78853
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The present invention relates to a new method of assaying for a compound which may protect stratified squamous epithelia from damage by a noxious substance. The method of the invention involves determining the level or presence of an interaction between the test compound and a polypeptide sequence comprising a portion of the extracellular domain of the junctional protein E-cadherin or a related polypeptide sequence. The method is useful for identifying compounds, which may protect stratified squamous epithelial tissue against injury by noxious substances. In particular, the method is useful for identifying compounds for protective effects against luminal damaging compounds or compounds for protective useful in treating conditions associated with gastric influx e.g.
                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 51-53; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compounds that protect stratified squamous epithelial tissue against injury by noxious substances, by determining interaction between a test compound and an E-cadherin extracellular domain
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## ALIGNMENTS

US/09323427

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; ORGANISM: Dirofilaria immitis US-09-323-427-4
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APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: COPERATION FOR A COUNTY OF THE PARAMETERIOR OF A CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
EEARLIER FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 387
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Best Local Similarity
Matches 387; Conserva
                                                                                                                                        SAEPENIIDVRTDINTLEISDDNQALFVDLRHRALLQHNGQFVILAAVQNGICMSFFGFS
                                                                 EGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQ 120
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RESULT 3
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US-09-812-642-4
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Best Local S
Matches 387
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                                                                                                                                          Sequence 17, Application US/09323427 Patent No. 6248329
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
LENGTH: 387
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APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins,
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/323,427
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 60/087,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
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TYPE: PRT
ORGANISM: Dirofilaria immitis
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PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 245
TYPE: PRT
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US-09-323-427-17
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Best Local S
Matches 195
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Patent No. 6368600
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 17
LENGTH: 245
TYPE: PRT
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Best Local Similarity
Matches 195; Conserv
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic
TITLE OF INVENTION: Molecules, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
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                                                                                 Local Similarity 80.6 es 195; Conservative
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                                                                                                                                                            CDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYK
                           FYMEADKTVSTQIEVSEMTTVFATQLVPMPVCRYEILDGGPTGQPVQYANIGQPVYHKWT
                                           FYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWT 181
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                                                                                                                                                                                                   53.6%; Score 1086.5; DB 4; 80.6%; Pred. No. 3.8e-120; tive 24; Mismatches 22;
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; TYPE: PRT
; ORGANISM: Dirofilaria immitis
US-09-323-427-9
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                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09812642 Patent No. 6368600 GENERAL INFORMATION:
                                                                      CURRENT APPLICATION NUMBER: US/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 9
LENGTH: 271
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LENGTH: 271
TYPE: PRT
ORGANISM: Dirofilaria immitis
-09-812-642-9
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APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic
TITLE OF INVENTION: Molecules, and Uses Thereof
                                                                                                                                                                                            FILE REFERENCE: HW-8
                                                                                                                                                                                                                      APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitle Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
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DNTVDVSTGFSTVDITEEN 213
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RESULT 7
US-07-707-367-2
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Best Local Similarity
                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 141678/90
FILING DATE: 01-JUN-1990
PRIOR APPLICATION NUMBER: JP 210535/90
FILING DATE: 10-AUG-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                          TELEFAX: (919)541-8689 INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                              SEQUENCE CHARACTERISTICS:
LENGTH: 935 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                 APPLICATION NUMBER: JP 329911/90
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Villamizar, JOAnn
REGISTRATION NUMBER: 30,598
                                                                                                                                          REFERENCE/DOCKET NUMBER: 4-
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kangawa, Kenji
TITLE OF INVENTION: No. 5196316el Enzyme and DNA Coding Therefor
NUMBER OF EEQUENCES: 2
CODECCONTENCE: 2
CODECCONTENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CIBA-GEIGY CO
STREET: 7 Skyline Drive
                   TOPOLOGY:
                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Nishikawa, Yoshiki
Kawahara, Takashi
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Suzuki, Kenji
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                                                                                                                               (914)785-7120
protein
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72.4%;
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US-08-070-301-16
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
PRIOR APPLICATION DATA:
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                               FILING DATE: 24 CLASSIFICATION:
                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20036-8218
                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                      STREET:
            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       KISHIMOTO, Jiro
IFUKU, Ohji
KATO, Ichiro
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OKAMOTO, Hiroshi
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                                                                                                               24-MAY-1991
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                                                                                                                             us/08/070,301
              JP 1-181933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 835-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE,
                                                                                                                                                                  APPLICANT: RAMBOSEK, JOHN
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Fro
                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVY 240
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                                                                                           CITY:
                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 RGIFV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 2 FILING DATE: 02-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 2-
FILING DATE: 26-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QIKHQEFGREVFAVSYAP------GG-----VLYAVNGKPYYG----DSTPVQGF
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50; Conservative
                                                                                          RAHWAY
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                                                                                                                                                                                                                          CONDER, MICHAEL J.
MCADA, PHYLLIS C.
REEVES, CHRISTOPHER D.
DAVIS, CHARLES R.
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21.6%; Pre
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Pred. No. 0.074;
Prematches 66;
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                                                                                                         P.O.
                                                                                                         Box 2000
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; Sequence 2, Application US/08637640
Patent No. 5849541
GENERAL INFORMATION:
APPLICANT: VINCI, VICTOR A.
APPLICANT: CONDER, MICHAEL J.
APPLICANT: MCADA, PHYLLIS C.
APPLICANT: REEVES, CHRISTOPHER D.
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US-08-637-640-2
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TELEPHONE: 908-594-6734
TELEPHONE: 908-594-4720
TELEPHONE FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,332
                                                                                                                                                                                                                                                           1529 KTMAHARSLIKPGGQMVILEITHKEHTRLGFIFGLFADWWAGVDDGRCTEPF 1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1175 VAFQTVIGA--YSSP-----GDRRLRCLYVPTHVDRITLVPSLCLATAESGCEKVAFNT 1226
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NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     1442 ILEI------------GAG---TGGATKYVLATPQLGFNSYTYTDI 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1283 PDSLLDNPEYWATAQDKEAIPIIERIYYFYI---RSFLSQLTLEERQQAAFHLQKQIEWL 1339
                                                                                                                                                                                                                                                                                                                                                 1473 STGFFEQAREQFAPFEDRMVFEPLDIRRSPAEQGFEP-HAYDLIIASNVLHATPD---LE 1528
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                                                                                                                                                                                                                                                                                    245 RSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQL-------
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STRANDEDNESS: si
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               VINCI, VICTOR A.
CONDER, MICHAEL J.
MCADA, PHYLLIS C.
REEVES, CHRISTOPHER D.
DAVIS, CHARLES R.
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1528	STGFFEQAREQFAPFEDRMVFEPLDIRRSPAEQGFEP-HAYDLIIASNVLHATPDLE	1473	дЬ	
327	RLLKKRSAEPENIIDVRTDINTLEISDDNQALP	295	Qy	
1472	ILEIGAGTGGATKYVLATPQLGFNSYTYTDI	1442	ДЪ	
294	RSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQL	245	Qy	
244 1441		202 1384	Оy	
1383	EQVLASAKEGRHLWYDPGWENDTEAQIEHLCTANSYHPHVRLVQ	1340	뫄	
201	PYCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDD::	151	QΥ	
1339	RSFLSQLTLEERQQAAFHLQKQIEWL	1283	рb	
150		99	φ	
1282	LTG	1227	Дb	
86	DOEGCRNDEGGRQVAGISL-PFDSCNVARTRSLNPRGIFVT	45	Qy	
1226	VAFQTVIGAYSSPGDRRLRCLYVPTHVDRITLVPSLCLATAESGCEKVAFNT	. 1175	Db	
44	DNGVEGEPEIECGPTSITINFNT	6	Qy	
sd	Match 4.3%; Score 87; DB 2; Length 3038; Local Similarity 19.7%; Pred. No. 6.7; Local Similarity 55; Mismatches 138; Indels 186; Gaps	Query M Best Lo Matches	2 111 0	
	ORGANISM: TPKS Protein 37-640-2	OR 08-637	us-	
	ũ	ORIG	<b></b> .	
	- P	MOLE		
	STRANDEDNESS: single TOPOLOGY: linear	TO	·. ·.	
	TYPE: amino acid	TY	٠. ٠	
	HARACTERISTICS:	SEQUENCE C		
	TELEFAX: 908-594-4720 RMATION FOR SEO ID NO: 2:	INFORM		
	TELEPHONE: 908-594-6734			
	REFERENCE/DOCKET NUMBER: 19076	TELE		
	တွင်	RE	٠. ٠	
	AGENT INFORMAT	ATTO		
	APPLICATION NUMBER: 08/148/132 FILING DATE: 01-NOV-1993	FI AP	٠. ٠.	
	APPLICATION DATA:	PRIOR	٠. ٠	
	G-1996	유립		
	APPLICATION DATES	CURRENT		
	ARE: PatentIn Re	SO		
	OPERATING SYSTEM: PC-DOS/MS-DOS	90		
	TYPE: Flop	ME		
	ZIF: U/U05 COMPUTER READABLE FORM:	COMP	•• ••	
	) K	0.0		
	CITY: KAHWAY STATE: NJ	ST	٠. ٠.	
	.o. BOX 2000; 12	TS	٠. ٠	
	SSEE: CHRISTINE F	CORR		
	SEQUENCES: 3	NUMBER		
		APPLICANT		
		APPL		

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US-09-004-406C-2
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SEQ ID NO 2
LENGTH: 30:
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Matches
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APPLICANT: Vinci, Victor A.
APPLICANT: Conder, Michael J.
APPLICANT: McAda, Phyllis C.
APPLICANT: Reeves, Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hendrickson, Lee E.
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE
FILE REFERENCE: 19076PDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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     1529
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KTMAHARSLLKPGGQMVILEITHKEHTRLGFIFGLFADWWAGVDDGRCTEPF 1580
                                      VDLRH-RALLQHNGQPVIL--
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                                                                                                                                                                                                                                                                                                                                       PVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDD------
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                                                                          STGFFEQAREQFAPFEDRMVFEPLDIRRSPAEQGFEP-HAYDLIIASNVLHATPD---LE
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19.7%; Pred. No.
ative 55; Mismatc
                                                                                                             -----RLLKKRSAEPENIIDVRTDINTLEISDDNQALP 327
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                                                                                                                                                  GAG---TGGATKYVLATPQLGFNSYTYTDI 1472
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                                     --- AAVQNGICMSPF
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RESULT 12 US-09-134-001C-3139

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; MOLECULE TYPE: US-08-682-517-15
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LENGTH: 438
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08682517 Patent No. 5874267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                          CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                            SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,517
                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXNUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
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                                                                                                                                                                                            COMPUTER: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                        TOPOLOGY:
                                                       TYPE:
                                                                    LENGTH:
                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-----CVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTL
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                                                     amino acid
                                                                      1222 amino acids
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                                                                                                                                                                                                                                                       Floppy disk
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19.2%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                              Expression of surface 25
                                                                                                                                                                  US/08/682,517
                                                                                                            15:
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DIAGNOSTICS
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US-08-682-517-9
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Best Local Similarity 19.8%;
Matches 72; Conservative 5
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LENGTH: 1252 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                         149
                                                                                                                                                                                                                                                           706 NQSGKKVTGTSIKKATYTIYNTGANDIKVDNQVISPNRSYTVTYEATLSSTGTVITPAKN 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             823 KYFGANGNEVFGEAAWEALL---TQYATE---GQKVTISYNVDGDTVTFKV---ISAVNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 LFVTKVD---------RAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 NQSGKKVTGTSIKKATYTIYNTGANDIKVDNQVISPNRSYTVTYEATLSSTGTVITPAKN 735
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                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.1%; Score 83; DB Local Similarity 19.8%; Pred. No. 4.4; Pred. No. 4.1%; Pred. No. 4.4;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 DEGGRQVAGISLPFDSCNVART-----RSLNPRGIFVTT-----TVVISFHP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
PMPVCRYEILDGGPTGQPVQEAIIGQ-PVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTV 207
                                                                                                          LEVTSVDGKTTAVKVIATGIAVNTDGKDYAFTA--KEATATFTATNEVPNSYTGVATQ---821
                                                                                                                                                                                                                                                                                                                                DEGGRQVAGISLPFDSCNVART-----RSLNPRGIFVTT-----TVVISFHP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADADLNVSATTVDTATVSLKDSANNSLSLTLVETGANTGVFATTVQAG-TLSSLTAGTLT 976
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Pred. No. 4.2;
                                                                                                                                                                                   -RAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
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                                                                                                                                                                                                                                                                                                                                                                                                            133;
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US-08-348-006B-5
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                                                                 Matches
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                                                                                                  Query Match
                                                                                                                                                                                                                                                    TELEPHONE: 908-594-391
TELEFAX: 908-594-4720
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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324 GTPMVTENTATSITITWDSGNPDPVSYYVIEYKSKSQDGPYQIKEDITTTRYSIGGLSPN 383
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CITY: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                    27 GEPEI-ECGPTSITINFNTRNAFEGHYYV------KGLY----DQECCRNDEGGRQ-- 71
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ZIP: 07065-0900
                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                 Similarity
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RUTLEDGE, SU JANE
IVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
IVENTION: TYROSINE PHOSPHATASE
                                                                 Conservative
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                                                                Score 81.5; D
Pred. No. 14;
17; Mismatches
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Best Local
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tent No. 5866397
                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-994-3905
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                            Local
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       27
                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                     FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: RAHWAY
STATE: NEW JERSEY
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GEPEI-ECGPTSITINFNTRNAFEGHVYV------KGLY----DQEGCRNDEGGRQ-- 71
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                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       07065-0900
                                                                                                                                                            1911 amino acids
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126 E. LINCOLN AVE., P.O. BOX 2000
                                Conservative
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                                            4.0%;
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                               47;
                                           Score 81.5;
Pred. No. 14;
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                             Mismatches 137;
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US-09-158-657-5
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                          TOPOLOGY:
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328 VDLRHRALLQHNGQPVILAAVQNGICMSPFG 358
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                                                                                                                                                          CSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENI--IDVRTDINTLEISDDNQALP
                                                                                                                                                                                                                                                                   DGCALD---KYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQ
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VSWRPPPPETHNG----ALVGYSVRYRPLG 650
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                                                                                                            ---PQGLGAF-----TPVVRQRTLQSKPSAPPQDVKCVSVR---
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; MOLECULE TYPE: US-09-158-657-5 Sequence 5, Application Patent No. 6214564 GENERAL INFORMATION: TELEFAX: 732-594-4720 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1911 amino acids FILING DATE: 14-FEB-1997 ATTORNEY/AGENT INFORMATION: NAME: HAND, J. MARK TELEPHONE: 732-594-3905 PRIOR APPLICATION DATA:
APPLICATION NUMBER: SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000 TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHATASE NUMBER OF SEQUENCES: TELEPHONE: /32-594-4720 STRANDEDNESS: REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18 CLASSIFICATION: FILING DATE: APPLICATION NUMBER: RAHWAY NEW JERSEY amino acid NSD RUTLEDGE, RODAN, GIDEON A. SCHMIDT, AZRIEL linear protein single US/09158657 SU JANE 08/800,825 US/09/158,657 ū 18992DA

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RESULT 18
PCT-US94-10166-5
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 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                     FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, JOHN W III
REGISTRATION NUMBER: 35403
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 09-SEPT-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RODAN, GIDEON A
APPLICANT: SCHAIDT, AZRIEL
APPLICANT: ROTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CDNA ENCODING A NOVEL TITLE OF INVENTION: TYROSINE PHOSPHATASE
                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444 LIRGYRYY-YTMEPEHPYGNWQKHNYDDSLLTTYGSLLEDETYTYRYLAFTSYGDGPLSD 502
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                                        TELEPHONE: 500 --- 908-594-4720
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 07065
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                                    TELEX: 138825
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: JOHN W. WALLEN III
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE
                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PQGLGAF-----TPVVRQRTLQSKPSAPPQDVKCVSVR---
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                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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%; Pred. No. 14;
47; Mismatches 137;
                                                                                                          18992
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO fOR WINDOWS VERSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,076
FILING DATE: 17-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5789217el tRNA Synthetase
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 96010
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
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                                 APPLICATION NUMBER:
                                                   FILING DATE:
                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
                  FILING DATE:
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                                               27-JUL-1996
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9615845.6

9601096.2

Beecham Corporation Road

9622617.0

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; MOLECULE TYPE: protein PCT-US94-10166-5
625 VSWRPPPPETHNG----ALVGYSVRYRPLG 650
                                                                                                           587 ---PQGLGAF----
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                                                                                                                                                                   270 CSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENI--IDVRTDINTLEISDDNQALP 327
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 GEPEI-ECGPTSITINFNTRNAFEGHVYV------KGLY----DQEGCRNDEGGRQ-- 71
                                                                                                                                                                                                                                                                                                                                                                                               PVQF----AIIGQPVYHKWTCDSETVDTFC-----AVV--HSCFVDDGNGDTVEILNA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VAGISL----PFDSCNVART------RSLNPRGIFVTTTVVISFHPLFVTK 112
                                                  VDLRHRALLQHNGQPVILAAVQNGICMSPFG 358
                                                                                                                                                                                                                                                                                                                                            PIQVKTQQGVPGQPMNLRAEARSETSITLSWSPPRQESIIKYELLFREGDHGREV-----
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21.5%;
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s; Pred. No. 14;
47; Mismatches 137;
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 FILING DAY...
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,076
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 9601096.2
APPLICATION NUMBER: 9615845.6
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Best Local Similarity 15...
55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                   SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018 074
FILING DAMPS.
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NO. 6410286el tRNA Synthetase NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 VISFHPLFVTKVDRAYR--VQCFYMEADKTVSAQIEVSEITTAFQTQIVP--MPVCRYEI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 --PQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQALPVDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 LDGGPTGQPVQFAIIGQPVYHKWTCDSETVDT-FCAVVHSCFVDDGNGDTVEILNADGCA 216
                                                                                                                                                                                              COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                 CITY: King of Prussia
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TOPOLOGY: lir
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Pred. No. 1.4;
16; Mismatches 103;
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RESULT 21
US-08-785-076-2
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Best Local
                                             CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08,
FILING DATE: 17-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19-JAN-
APPLICATION NUMBER:
                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hodgson, John APPLICANT: Lawlor, Elizabeth TITLE OF INVENTION: No. 5789:
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wi
                                                                                                                                                                                                                                                                    STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                        ZIP: 19406-0939
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 430 LENGTH: A30 LENGTH: A30 LENGTH: A30 LENGTH: A31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRYGSVPH-----C----GFGLGLERTVAWISGV 412
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                   19-JAN-1996
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for Windows Version
                                                                                                      US/08/785,076
                                 9601096.2
   9615845.6
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Pred. No. 1.4;
46; Mismatches
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DATE:

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RESULT 22
US-09-018-824-2
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                                                                                                                                                                   COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7/
FILING DATE: 17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
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                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6410286el tRNA Synthetase
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                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                  CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                    CLASSIFICATION: 435
                                                                     FILING DATE:
                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 432 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRYGSVPH-----C----GFGLGLERTVAWISGV 414
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                                                                                                                                                    IBM Compatible
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Pred. No. 1.4;
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; Sequence 20, Application US/08484575A
; Patent No. 5925358
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SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acid
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,575A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of t
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mark D. Cochran and David E. Junker TITLE OF INVENTION: Recombinant Fowlpox Viruses
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CLASSIFICATION:
ATTORNEY/AGENT INI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 RRYGSVPH------C----GFGLGLERTVAWISGV 414
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APPLICATION NUMBER: 96226
APPLICATION TATE: 30-007-1996
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                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                         CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIALIAAV
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                                                                                                                                                                                                                       New York
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INFORMATION:
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Pred. No. 1.4;
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RESULT 24
US-08-477-459-20
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Best Local Similarity 10...
80; Conservative
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INFORMATION FOR SEQ ID NO:
          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/477,459
                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                           APPLICANT: Mark D. TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 VWSI 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 IITI 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 DDEVPEDTEHDDPNSDPDYYNDMPAVIPVEETTKSSNAVSM-PI-FAAFVACAVALVGLL
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                                                                                                                                       COUNTRY: UZIP: 10036
                                                                                                                                                                        CITY: New York
STATE: New York
FILING DATE:
                                                                                                                                                                                                            STREET:
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                                                                                                                                                        USA
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(212)391-0525
07-JUN-1995
                                                                                                                                                                                                                                                                                                                 Cochran
                                                                                                                                                                                                                                                                             Recombinant Fowlpox Viruses and Uses Thereof
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Pred. No. 2.5;
5; Mismatches 148;
                                                                                                                                                                                                              Americas
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RESULT 25
US-08-479-869-20
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                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08479869 Patent No. 6123949
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                        STREET: JUST
STREET: New York
CITY: New York
CTATE: New York
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                    APPLICANT: Cochran Ph.D, Mark D
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
TITLE OF INVENTION: Uses Thereof
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NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           425 VWSI 428
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                                                                                                             COUNTRY: UZIP: 10112
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80; Conservative
                                                                                                                                                                                   30 Rockefeller Plaza
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18.9%; Pred. No. 2.5;
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                    Version #1.25
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CURRENT APPLICATION NUMBER: US/08/486,414B
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 434
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                       Sequence 46, Application US/08486414B Patent No. 6136318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%;
Best Local Similarity 18.9%;
Matches 80; Conservative 5
                                                                                                                       APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUSES
FILE REFERENCE: 42771D
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NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
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TYPE: amino acid
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                                                                                                                                           AND
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RESULT 27
PCT-US94-01826A-20
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GENERAL INFORMATION:
APPLICANT: Syntro Corporation, et a
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Best Local Similarity
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                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Syntro Corporation, et al TITLE OF INVENTION: Recombinant Fowl
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                                                                                                                                                                                       APPLICATION NUMBER: PCT/
FILING DATE: 28-FEB-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                          TELEX: 422523
                                                                                           TELEFAX:
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PCT-US94-02252A-20
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GENERAL INFORMATION:
APPLICANT: Syntro Corporation, et al.
TITLE OF INVENTION: Recombinant Fowlpox Viruses
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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Best Local Similarity 18.9
Matches 80; Conservative
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 434 amino acids
                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02252A
FILING DATE: 28-FEB-1994
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                     STREET: 30 Roc
CITY: New York
                                                                                       TELEPHONE:
                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                    New York
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                                                                  (212)977-9550
(212)664-0525
                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application PC/TUS9603916
GENERAL INFORMATION:
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Mark D.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity 18.9%;
                                                                                                                                                COMPUTER: TEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.22 CURRENT APPLICATION DATA:
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 24-SEP-
                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                 FILING DATE: 2
CLASSIFICATION:
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REGISTRATION NUMBER:
                   NAME:
                                                                                                                                  APPLICATION NUMBER:
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Pred. No. 2.5;
55; Mismatches
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INFORMATION FOR SEQ ID NO: 1
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.29
                                                                                                                                                                                                                                                                                        APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 39116-A TELECOMMUNICATION INFORMATION:
              SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/039:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                   STREET: 1185 AVE
CITY: New York
STATE: New York
COUNTRY: U.S.A.
21P: 10036
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                                                                                                                                                                                                                                ADDRESSEE: Cooper & Dunham STREET: 1185 Avenue of the
FILING DATE:
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23-MAR-1995
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              PCT/US96/03916
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RESULT 31
US-08-484-993B-16
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                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                            Sequence 16, Application US/08484993B Patent No. 5837497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                        APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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PRIOR APPLICATION DATA:
                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 LV-SRNGAGLTIFSPTAALSGQYLLTLKIGRFAQTALVTLEVNDRCLKIGSQLNFLPSKC 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 PYNRYLTRVSRG----CDVVELNPISNVDDMISAAKEKEK------141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 CSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQA----
                                                             STREET: 6300
CITY: Chicago
COUNTRY: United States of America ZIP: 60606-6402
                                            STATE:
                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/126,597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SVPQEIPAVTKKAEGRTPDAES-----SEKKAPPE---DSEDDMQA-EASGENPAALPE 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 3.9%; l Similarity 18.9%; 80; Conservative 5
                                       Illinois
                                                                               E: Marshall, O'Toole, 6300 Sears Tower, 233
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%; Pred. No. 2.5;
55; Mismatches 148; Indels 141;
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                                                                                 Gerstein, Murray &
South Wacker Drive
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; MOLECULE TYPE:
US-08-484-993B-16
                                                                                                                                                                                                                           Sequence 16, Application US/08484158B Patent No. 5976545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                            APPLICANT: Harris Ph.D., Jeffrey APPLICANT: Hsu, Kuang T. APPLICANT: Podolski, Joseph S. TITLE OF INVENTION: Pharmaceutic TITLE OF INVENTION: Immunocontra NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
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APPLICATION NUMBER:
FILING DATE: 29-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           377 LRDPIYVEVSIRHRTDPSLGLLLHNCWATPGKNSQSLSQWPIL-VKGC---PYVGDN--Y
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                                                                                                                                                                                                                                                                                                                                    431 QTQLIPVQKALDTPFPSYYKRFSIFTFSFVDTMAKWALRGPVYLHCNVSICQPAGTSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 SVRSNAFPLSVQVFTIPPPHLKTQHGPLTLELKIAKDKHYGSYYTIGD-----YPV-VKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 MEADKTVSAQIEVSEITTA-FQTQIVPMPV-----CRYEILDGGPTGQPVQFAI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 FSIAVSRNVTSPP------LLLN-SLRLAFG-----KDRE-CNPVKATRAFALFF 271
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MEDIUM TYPE: Floppy disk
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 LPEDSCNVARTRSLNPRGIEVTTTVVISFHPLFVTKVDRAY------RVQCFY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Clough, David W.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                      Harris Ph.D., Jeffrey D.
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312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%;
21.1%;
                                                                                                             Immunocontraception
                                                                                                                              Pharmaceutical Compositions for
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ER: 31745
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Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                       ------HVYKYADRSQLFYQCQISITIKEPNSEC 265
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                                                                                                                                                                                                                  RESULT 33
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                                                                                                                                                     Sequence 16, Application US/08484596A
Patent No. 5981228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.1
Matches 63; Conservative
                                                   GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
APPLICANT: Podolski, Materials and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                     NUMBER OF SEQUENCES: 5
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
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PRIOR APPLICATION NIMBER: 07/973,341
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PRIOR APPLICATION NUMBER: 08/149,223
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                       431 QTQLIPVQKALDTPFPSYYKRFSIFTFSFVDTMAKWALRGPVYLHCNVSICQPAGTSSC 489
                                                                                                                                                                                                                                                                                                                                                                                 172 IGQPVYHKWTCDSETVDTFCAVVHSCFVDDG-NGDTVE---ILNADGCALDKYLLNNLEY 227
                                                                                                                                                                                                                                                                                                                                                                                                                            323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGIS 76
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TELEPHONE: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07
FILING DATE: 09-NOV-92
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                                                                                                                                                                                                                                                                                                          PTDLMAGQEA -----
                                                                                                                                                                                                                                                                                                                                             LRDPIYVEVSIRHRTDPSLGLLLHNCWATPGKNSQSLSQWPIL-VKGC---PYVGDN--Y 430
                                                                                                                                                                                                                                                                                                                                                                                                                        SVRSNAFPLSVQVFTIPPPHLKTQHGPLTLELKIAKDKHYGSYYTIGD-----YPV-VKL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPFNSCGTTR------WVTGDQAVYENELVAARDVRTWSHGSITRDSIFRLRVSCSY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                       Podolski, Joseph S.
VENTION: Materials and Methods for EQUENCES: 59
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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21.1%; Pred. No. 4;
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                                                                                                                                                                                                                                                                                                        -----HVYKYADRSQLFYQCQISITIKEPNSEC 265
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                                                        Immunocontraception
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                                                                                                                                                                                     RESULT 34
US-08-480-150A-16
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                                   Sequence 16, Application US/08480150A
PATENT NO. 5989550
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: HSU, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/1.
FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
FILING DATE: 09-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6653
                                                                                                                                                                                                                                                                   431 QTQLIPVQKALDTPFPSYYKRFSIFTFSFVDTMAKWALRGPVYLHCNVSICQPAGTSSC
                                                                                                                                                                                                                                                                                                                                                                                  172 IGQPVYHKWTCDSETVDTFCAVVHSCFVDDG-NGDTVE---ILNADGCALDKYLLNNLEY 227
                                                                                                                                                                                                                                                                                                                                                                                                                       323 SVRSNAFPLSVQVFTIPPPHLKTQHGPLTLELKIAKDKHYGSYYTIGD-----YPV-VKL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 LPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAY-------RVQCFY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGIS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Marshall, O'Toole, Gerstein, Murray & Borun
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Pred. No. 4;
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RESULT 35
US-08-458-731-16
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                                                                                                          Patent No.
                                                                                                                             Sequence 16,
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Best Local Similarity
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                         GENERAL INFORMATION:
                                APPLICANT:
APPLICANT:
APPLICANT:
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                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    431 QTQLIPVQKALDTPFPSYYKRFSIFTFSFVDTMAKWALRGPVYLHCNVSICQPAGTSSC
                                                                                                                                                                                                                                                          228 PTDLMAGQEA----
                                                                                                                                                                                                                                                                                                                                                                323 SVRSNAFPLSVQVFTIPPPHLKTQHGPLTLELKIAKDKHYGSYYTIGD-----YPV-VKL 376
                                                                                                                                                                                                                                                                                                                                                                                                   124 MEADKTVSAQIEVSEITTA-FQTQIVPMPV------CRYEILDGGPTGQPVQFAI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                          272 FPFNSCGTTR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATALE 09-NU. - FILING DATE: 09-NU. - 08/01 APPLICATION NUMBER: 08/01 APPLICATION TATE: 29-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US US TITLING DATE: 09-NOV-1993
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                            IGQPVYHKWTCDSETVDTFCAVVHSCFVDDG-NGDTVE---ILNADGCALDKYLLNNLEY 227
                                                                                                          6, Application US/08458731 6001599
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Hsu, Kuang T.
Podolski, Joseph S.
INTERVITION: Materials and Methods for Immunocontraception
QUENCES: 59
                                                                    Harris Ph.D., Jeffrey D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9%; Score 78.5; 1
21.1%; Pred. No. 4;
tive 38; Mismatches
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RESULT 36
US-08-149-223A-16
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                                                                                 Sequence 16, Application US/08149223A Patent No. 6027727 GENERAL INFORMATION:
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
                                                                                                                                                                                        431 QTQLIPVQKALDTPFPSYYKRFSIFTFSFVDTMAKWALRGPVYLHCNVSICQPAGTSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/97 FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 323 SVRSNAFPLSVQVFTIPPPHLKTQHGPLTLELKIAKDKHYGSYYTIGD-----YPV-VKL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/01
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
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ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGIS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clough, David W.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OFILING DATE: 09-NOV-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                            PTDLMAGQEA----
                                                                                                                                                                                                                                                                                                                                              MEADKTVSAQIEVSEITTA-FQTQIVPMPV------CRYEILDGGPTGQPVQFAI 171
                                                                                                                                                                                                                                                                                                                                                                             FPFNSCGTTR------WVTGDQAVYENELVAARDVRTWSHGSITRDSIFRLRVSCSY 322
                                                                                                                                                                                                                                                                                                                                                                                                            LPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAY------RVQCFY 123
                                                                                                                                                                                                                                                                                  IGOPVYHKWTCDSETVDTFCAVVHSCFVDDG-NGDTVE---ILNADGCALDKYLLNNLEY 227
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Pred. No. 4;
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South Wacker Drive
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RESULT 37
US-08-325-071-61
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                                                                    Sequence 61, Application US/08325071 Patent No. 5587311 GENERAL INFORMATION:
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Best Local Similarity
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     APPLICANT:
                                      APPLICANT:
                                                  APPLICANT:
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FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           431
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                                                                                                                                                                                                                         228 PTDLMAGQEA---
                                                                                                                                                                                                                                                                                   172 IGQPVYHKWTCDSETVDTFCAVVHSCFVDDG-NGDTVE---ILNADGCALDKYLLNNLEY 227
                                                                                                                                                                                                                                                                                                                               323
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TELEFAX: 25-3856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGIS 76
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CLASSIFICATION:
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                                                                                                                                                                                 QTQLIPVQKALDTPFPSYYKRFSIFTFSFVDTMAKWALRGPVYLHCNVSICQPAGTSSC
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                                                                                                                                                                                                                                                                                                                      SVRSNAFPLSVQVFTIPPPHLKTQHGPLTLELKIAKDKHYGSYYTIGD-----YPV-VKL
                                                                                                                                                                                                                                                                                                                                                                                       FPFNSCGTTR------WVTGDQAVYENELVAARDVRTWSHGSITRDSIFRLRVSCSY
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                 COBON, Stewart Gary
MOORE, Joanna Terry
JOHNSON, Law Anthony York
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WILLADSEN,
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312/474-0448
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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21.1%;
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fower, 233
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Pred. No. 4;
38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
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APPLICATION NUMBER: 1
FILING DATE: 27-NOV-
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APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membran
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                           115 RAYRVQC----FYMEADKTVSAQIEVSEITTAFQTQIV-PMPVCRYE---ILDGGPTGQPV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: AU PI2570
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                                                                                                                                          146 KAYECTCPRGFTVAEDGITCKSISHTVSCTAEQKQTCRPTEDCRVHKGTVLCECPWNQ-- 203
                             212 ADGCALDKYLLN-----NLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECV 266
                                                                                                      168 QFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDG-------NGDTVEILN 211
250 INGCLLNEYYYTVSFTPNISFDSD-----HCKWYEDR--VLEAIRTSIGKEVFKVEIL
                                                                                                                                                                                                                Local Similarity les 62; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202 672 5399
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                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                      protein
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                                                                      -TCISDCVDKKC---HEEFMDCGVYMNRQSCYCPWKSRKPGPNV---N
                                                                                                                                                                                                                                 3.8%; Score 78; I
23.4%; Pred. No. 4.
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                                                                                                                                                                                                                                                Length 549;
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              TELEX: 904136
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
SEQUENCE CHARACTERISTICS:
                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
                                                                                                                                                                                                                FILING DATE: 16-OCT-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P.
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PRIOR APPLICATION NUMBER: 07/242,196
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APPLICATION NUMBER:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA Encoding A Cell Membra TITLE OF INVENTION: Glycoprotein Of A Tick Gut
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                                                                                                                                                                   FILING DATE: 19-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                         TELEPHONE: ZUZ
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STREET: 30
                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
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                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILLADSEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                  AU PI4912
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-461-004A-61
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US-08-325-071-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                             PRIOR APPLICATION DATA:
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/926,368
                                                                                                                                                FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
                                                                                                                                                                                                                                  SOFTWARE: Patentin Rela
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DNA Encoding A Cell Membrane TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WILLADSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 ENLCDSLLKNQEAAYKGQNKCVKVD 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 ADGCALDKYLLN-----NLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 --HLVGD-----TCISDCVDKKC---HEEFMDCGVYMNRQSCYCPWKSRKPGPNV---N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 KAYECTCPRGFTVAEDGITCKSISHTVSCTAEQKQTCRPTEDCRVHKGTVLCECPWNQ--
                                                                                               APPLICATION NUMBER: US 07 FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000 K Street, CITY: Washington, D.C.
APPLICATION NUMBER: PCT/AU87/00401 FILING DATE: 27-NOV-1987
                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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les 62; Conserv
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5587311
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                                                                                                                                                                                                                                                                                                                                                                                      3000 K Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COBON, Stewart Gary
MOORE, Joanna Terry
JOHNSON, Law Anthony York
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RAND, Keith No. 5587311man
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RESULT 40
US-08-461-004A-63
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                 APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrar
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
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REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
COMPUTER READABLE FORM:
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LENGTH: 650 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 19-JUN-PRIOR APPLICATION DATA:
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                                        COUNTRY:
                                                          CITY: Washington, D.C.
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Joanna Terry
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23.4%; Pred. No. 5
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILIG DATE: 04-JUN-1995
DEFOR SOFTWARE: 04-JUN-1995
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FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
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FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
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TELEFAX: 202 672 5399
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APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
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FILING DATE: 27 NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
BEFERENCE LOCKETS NUMBER: 29,768
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APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
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                                          305 ENIIDVRTDINTLEISDDNQALPVD 329
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TYPE: amino acid
TOPOLOGY: linear
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ENLCDSLLKNQEAAYKGQNKCVKVD 459
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: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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SEITTAFQTQIVEMPVCRYEILDGGPTGQEVQFAIIGQEVYKK 	GCRNDEGGROVAGISLÞEDSCNVARTRSLNÞRGIFVTTTVVISFHÞI 	NGVEGEPEIECGPTSITINENTRNAFEGHYYVKGLYDQ 	; Score 2026; DB 9; ; Pred. No. 1.1e-201; 0; Mismatches 0;	10054562A  H. H. H. E. HELMINTH CUTICLIN PROTEINS OF  1 US/10/054,562A  -06-10 09/812,642 09/812,642 09/323,427 -01 3.1	ALIGNMENTS	US-09-864-761-46862 US-09-870-759-128 US-09-802-640-32 US-09-989-240-32 US-09-989-293A-124 US-09-989-735-124 US-09-989-735-124 US-09-989-736-124 US-09-990-436-124 US-09-991-181-124 US-09-991-81-124 US-09-991-81-124 US-09-993-687-124 US-09-993-687-124 US-09-993-667-124 US-09-993-67-124 US-09-993-67-124 US-09-993-67-124 US-09-993-67-124 US-09-993-667-124 US-09-993-667-124 US-09-990-438-124 US-09-990-438-124 US-09-990-438-124 US-09-997-666-124
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CURRENT APPLICATION NUMBER: US/10/054,562A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/812,642
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VETSION 3.1
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                                                                Sequence 9, Application US/10054562A Patent No. US20020165375A1 GENERAL INFORMATION:
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patent No. US20020165375A1
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 195;
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: HW-8-2
CURRENT ADDITION:
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ORGANISM: Brugia malayi
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mes 195; Conservative
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                                                                                                                                                                                                                                                                                                                                       FYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWT 181
                                                                                                                                                                                                                      YA 243
                                                                                                                                                                                                                                                     CDSETYDTFCALVHSCFYDDGNGDSINLINEEGCALDRYLLNNLEYPTDLMAGQEAHVYK 243
                                                                                                                                                                                                                                                                                                                     FYMEADKTVSTQIEVSEMTTVFATQLVPMPVCRYEILDGGPTGQPVQYANIGQPVYHKWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQICSFLSYMIIASINAIPIDNGVESEPEIECGPTSITVNFNTRNPFEGHVYAKGLYSNQ
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               MOLECULES,
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US-09-923-563A-1
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; CURRENT APPLICATION NUMBER: US/10/054,562A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/812,642
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 09/323,427
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
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Best Local Similarity
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LENGTH: 271
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CURRENT APPLICATION NUMBER: US/09/923,563A
CURRENT FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bayer AG
APPLICANT: Wambach, Wolfga
TITLE OF INVENTION: Method
TITLE OF INVENTION: Thereo
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TYPE: PRT
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 196
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                                                                                                         AIDRTDEI---HPENVWICQRAARIIGLDIAGIDVVSPDISQPLSKVGGVIVEVNAAPGFR
                                                                                                                                               FVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIE-----VSEITTA--FQ 144
                                                                                                                                                                                     TRIEVNHDTWTLLEKQGYTLNTVLQPG-------EICYLRATANLSTGGI 398
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                                    MHTNPSQGIARNVAEPVLNMLFPPGTPCRIPI-FAITG-----TNGKTTTT-RLIAH
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Method for Improved Production of Cyanophycin and Secondary Pr
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22.0%; Pred. No. 1.3;
7ative 44; Mismatches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 474
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PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR EILING DATE: 1998-11-06
PRIOR PRIOR FILING DATE: 1998-10-13
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
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CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
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APPLICANT: Gayle II, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct of human CD39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                             114 IPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEG
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220 TFVPQNQTIE----SPDNALQFR 238
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Local Similarity 20.9%;
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                                                                             AYGWITINYLLGKFSQKTRWF----SIVPYETNNQ--
                                    AAAAQLRLLKKRSAEPENIIDVR 311
                                                                                                                                                                                                                                                                                                                             IDRMQLLSCIALSLALVTNSASTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYI--
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                                                                                                                  -KYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKP 288
                                                                                                                                                                                                    -GDT--VEILNADGCALDKYLLNNLE-----YPTD-----LMAGQEAH 238
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Pred. No. 1.
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; OTHER INFORMATION: Description of Artificial Sequence: Fusion ; OTHER INFORMATION: construct of human CD39 US-09-835-147-29
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PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
PRIOR APPLICATION NUMBER: DS 60/149,010
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                    Sequence 42, Application US/09909567B Publication No. US20030022257A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09835147 Patent No. US20020002277A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                 TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes FILE REFERENCE: DEX-0214 CURRENT EPPLICATION NUMBER: US/09/909,567B CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                     APPLICANT: Macina, Roberto
APPLICANT: Nair, Manoj
APPLICANT: Chen, Seiyu
                    PRIOR APPLICATION NUMBER: 60/219,834 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
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SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
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                                                                                                                                                                                                                                                                                                                                                                                            220 FVPQNQTIE----SPDNALQFR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                       290 AAAQLRLLKKRSAEPENIIDVR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 PRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ----YKWPAEKEN-DT--GVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IDRMQLLSCIALSLALVTNSSTKKTQLTSSTQNKALPENVKYGIVLDAGSSHTSLYI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGWITINYLLGKFSQKTRWF----SIVPYETNNQ---
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19.5%; Pred. No.
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1.6;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PAtentin ver. 3.0
SEQ ID NO 4320
LENGTH: 2069
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4320
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; LENGTH: 1118
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-909-567B-42
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Best Local Similarity 25.6%; Pred. No. 8.3;
Matches 52; Conservative 27; Mismatches 81;
                                                                                                                                                                                                                            Query Match 4.2%; Score 85; DB 9; Length 2069; Best Local Similarity 20.1%; Pred. No. 24; Matches 73; Conservative 50; Mismatches 116; Indels 1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
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                                            1489 RHCGHLDSEAGANSRWDHRPWCPHRYEQKEDTVSFALGRTLKTQGVLMLLP----- 1539
                                                                                                                                     1431 VSFVVPPDGHGKSWYLNDGFGIEHLPKVELRWLNLGIGNGQKRRLGGFEVTSPLFNV--C 1488
110 VTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 NGTYTVKIVAISEDYPRKTITGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLD 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 LDFSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVISIYVSESMD----R 403
                                                                                    64 R-----NDEGGRQVAGISLPF------DSCNVARTRSLNPRGIFVTTTVVISFHPLF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GGPTGQPVQFAIIGQP--VYHKW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 DRAYRYQCFYMEAD---KTVSAQ--IEVSEITTAFQTQIVPM-PVCR-----YEILD 159
                                                                                                                                                                                 15 LSYSIPVDN------GVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 LSYSIPVDNGVEGEPEI--ECGPTSITINFNTRNAFEG-----HVYVKGLYDQEGCR 64
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OCHIAI, KEIKO
YOKOI, HARGHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASAYO
OZAKI, AKIO
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                                                                                                                                                                                                                              Indels 124; Gaps
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ДУ	Оу	ОУ	Qу	Оy	Оy	Query M Best Lo Matches	US-09-	ဖ	GEN; AP; AP; AP; AP; AP;	RESULT 9 US-09-729- ; Sequence ; Patent N	рb	Qy	Db Oy	рb	Дb	Оу	
310 VRTDINTLEISDDNQALPVDLRHRALLQH 338 '	266VRPQCSEPQGFGAVKTGGAAAKPAAAAQLKLLKKKSAEPENI-ID 309	247QLFYQCQISITI 265	198 FVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRS- 246	147 IVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSC 197	87 TRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQ 146 	y Match 4.2%; Score 84.5; DB 10; Length 475; Local Similarity 18.8%; Pred. No. 2.9; Thes 62; Conservative 32; Mismatches 92; Indels 143; Gaps 12;	PE: PR GANISM GANISM ATURE: ME/KEY HER IN 729-45	REFERENCE: PC-0028 CIP ENT APPLICATION NUMBER: US/0 ENT FILING DATE: 2000-12-04 ER OF SEQ ID NOS: 32 WARE: PERL Program O NO 1	L INFORMATION: CANT: Lasek, Amy CANT: Krasnow, Ra CANT: Baughn, Mar CANT: Baughn, Mar	SULT 9 -09-729-454-1 Sequence 1, Application US/09729454 Patent No. US20020137038A1	1707 MLR 1709	335 LLQ 337	278 AVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQ-ALPVDLRHRA 334	230 DLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFG 277	1571DHLDVTSVQVPRTSGDGALDALLLH 1595	1540EYFGSEADSMVVTSL-IAAIKLGFREVLGGDP 1570 170 AIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPT 229	

RESULT 10

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US-09-137-531-9
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                                                                                                                                                        Sequence 9, Application US/09137531 Patent No. US20020048816A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.1%; Score 83; Best Local Similarity 19.8%; Pred. No. Matches 72; Conservative 50; Mismatc
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INFORMATION FOR SEQ ID NO:
                                                          TITLE OF INVENTION: Expression of surface
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676 NQSGKKVTGTSIKKATYTIYNTGANDIKVDNQVISPNRSYTVTYEATLSSTGTVITPAKN 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 LFVTKVD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        COMPUTER:
                        OPERATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                           VTY 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEIS- 320
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IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
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    Version #1.30 (EPO)
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 55, Application US/09808602
Patent No. US20020155115A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.1%;
Best Local Similarity 19.8%;
Matches 72; Conservative
              SOFTWARE:
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APPLICANT:
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APPLICANT:
                                                                                APPLICANT: MacDougall, John
TITLE OF INVENTION: NO. US20020155115A1el Proteins and
FILE REFERENCE: 15966-697 CIP
CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
                                                  PRIOR FILING DATE: 2000-03-03 NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1252 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 NSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEIS- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 KYFGANGNEVFGEAAWEALL---TQYATE---GQKVTISYNVDGDTVTFKV---ISAVNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 LFVTKVD--------RAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         706 NQSGKKVTGTSIKKATYTIYNTGANDIKVDNQVISPNRSYTVTYEATLSSTGTVITPAKN 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
NO 55
TH: 1948
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                                 PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                       Vernet,
                                                                                                                                                                                                                              Majumder, Kumud
Mishra, Vishnu
Mezes, Peter S
                                                                                                                                                                                                                                                                               Fernandes, Elma
Shimkets, Richard
Herrman, John L
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Pred. No.
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Same

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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5474
LEGID: 293
TYPE: PRT
                                                                        ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5474
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
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US-09-738-626-5474
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     Matches
                                     Query Match
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                   Local
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les 84; Conserv
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     31;
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                   IKEDA, MASATO
OZAKI, AKIO
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SENOH, AKIHIRO
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     Conservative
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                   3.9%;
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21.5%; Pred. No. 50;
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                 Score 80;
Pred. No.
   Mismatches
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                                   DB 9;
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   47;
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                                   Length 293;
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16;
Gaps
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FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: US 60/149,010
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US-09-835-147-8
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US-09-759-508B-2
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APPLICANT: Fishman, Mark C.
TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
FILE REFERENCE: 00786/381002
CURRENT APPLICATION NUMBER: US/09/759,508B
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/175,787
PRIOR APPLICATION NUMBER: US 60/175,787
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09835147 Patent No. US20020002277A1
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                                                                                                                                                                                                                     APPLICANT: Maliszewski, Charles R
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1130 DYEL-LMKSQQ------EMLYQTQVTAFVQEPEVGETAP-----GFVYSEYEKEY 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1076 LTTGYRYKVSYNKQTGECK-----LVISMTFADDAGEYTIVVRNKHGETSASASLLEEA 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 PLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.9%; Local Similarity 18.5%;
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Pred. No. 3.9e+03;
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PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 132
LENGTH: 299
TYPE: TERM
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                                                                       В
                                                                                                                                                                                                                       ; ORGANISM: HOMO Sapiens ; FEATURE: 
; NAME/KEY: misc_feature ; OTHER INFORMATION: Incyte ID No. US20020156263A1 3752346CD1 US-09-974-298-132
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US-09-974-298-132
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Best Local Similarity
Matches 52; Conserv
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NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VER: 2.0
SEQ ID NO 8
                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
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PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR FILING DATE: 1999-10-13
                                                                                                                                                                                                                                                                                                                  LENGTH: 29
TYPE: PRT
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                                189 TFCAVVHSCFVDDGNGDTVEILNADGCALD-----KYLLNNLEYPTDLMAGQEAHVYKYA 243
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                                                                                                                                                Local Similarity 22.7 es 57; Conservative
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                                                                                                         PMP-VCRYE--IL-----DGGPTGQPVQFAIIGQPVYH------KWTCDSETVD 188
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LFAKMEDTDFV----GWALDVLSPNLISTSMLGRVKYNLNSLSHDT-----ATGLIQYA 128
                                                                       PVPAVCRKEPCVLGVDEAGRGPVLGPMVYAICYCPLPRLADLEALKVADSKTLLESERER 78
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; Pred. NO. 9.5;
41; Mismatches
                                                                                                                                              Score 78.5; DB Pred. No. 5.9; 40; Mismatches
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-848-1
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Best Local
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 09/343,809
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                                                                                                                           149 PMP-VCRYE--IL-----DGGPTGQPVQFAIIGQPVYH-----
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   189 TFCAVVHSCFVDDGNGDTVEILNADGCALD-----KYLLNNLEYPTDLMAGQEAHVYKYA 243
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER: PCLA
APPLICATION 1998-07-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                               PVPAVCRKEPCVLGVDEAGRGPVLGPMVYAICYCPLPRLADLEALKVADSKTLLESERER 78
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1 Similarity 22.7%;
57; Conservation
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1999-12-01
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MRER: US 08/861,306
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BEP:
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; TYPE: PRT
; ORGANISM: Infectious Laryngotracheitis Virus
US-09-881-457A-4
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US-09-881-457A-4
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APPLICANT: Cochran, Mark D
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CURRENT APPLICATION NUMBER: US/09/881,457A
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/426,352
PRIOR TILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/804,372
PRIOR EPLICATION NUMBER: 08/804,372
PRIOR EPLICATION NUMBER: 08/804,372
PRIOR EPLING DATE: 1997-02-21
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PRIOR FILING DATE: 1995-08-09
PRIOR APPLICATION NUMBER: 08/63,566
PRIOR FILING DATE: 1996-06-13
PRIOR FILING DATE: 1996-08/288,065
PRIOR FILING DATE: 1994-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. US20020081316Alel Avian Herpes Virus and Uses Thereof
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                                                                                                                                    142
    223 -NNLEYPTDLMAGQEAHVYKYADRS--
                                       201 LV-SRNGAGLTIFSPTAALSGQYLLTLKIGRFAQTALVTLEVNDRCLKIGSQLNFLPSKC 259
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                                                                                                                                                                                                            106 PYNRYLTRVSRG----CDVVELNPISNVDDMISAAKEKEK-----
                                                                                                                                                                                                                                                                                          55 RNAMDRHLFLRNAFWTIVLLSSFASQSTAAVTYDY-----ILGRRALDALTIPAVG 105
                                                                                                                                                                                                                                                                                                                                  45 RNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVIS 104
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                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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FILING DATE: 1993-06-14
APPLICATION NUMBER: 08/023,610
FILING DATE: 1993-02-26
                                                                                                                                                                 DGGP-TGQPVQFAII----GQ----PVYHK--WTCDSETVDTFCAV------VHSC 197
                                                                                    FVDDGNGDTVEILNADGCALDKYLL-----
                                                                                                                         -GGPFEASYVWFYVIKGDDGEDKYCPIYRKEYRECGDVQLLSECAVQSAQMWAVDYVPST
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18.9%; Pred. No. 10
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5; Mismatches
-QLFYQCQISITIKEPNSECVRPQ 269
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; OTHER INFORMATION: Xaa -
US-10-121-746-10
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LENGTH: 646
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APPLICANT: Watter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. US20030036648Alel Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/10/121,746
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US/09/336,643A
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
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APPLICANT: Curran, Mark Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: H. sapiens
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  196
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                                                                                                                                                      92 RHVLNFYRTGRLHCPROECIOAFDEELAFYGLV----
                                                                                                                                                                                                                                 33 VKASRGDXVLVVNVSGRRFETW-KNTLDRYPDTLLGSSEKEFFYDADSGEYFFDRDPDMF 91
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                                                                                                           IIDVRTDINTLEISDDNQALPV--DLRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMG 364
IAVSVIANVVETI 208
                                     LSIALIAAVIITI 377
                                                                        AERLAED-EEAEQAGDGPALPAGSSLRQRLWRAFENPHTSTAAL-----VFYYVTGFF 195
                                                                                                                                                                                       -----TIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPEN 306
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                                                                                                                                                                                                                                                                                                                                    Score 77.5;
Pred. No. 24;
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
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Best Local
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LENGTH: 1706
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SOFTWARE: Annomax Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO ACO10872.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.1

OTHER INFORMATION: SWISSPROT HIT: P04114, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AA702484.1, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: AA702484.1, EVALUE 0.00e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                        256 CSLLV------LENELNAELGLSGASMKLTTNGRFREHNAKFSLDGKAALTELSL 304
                                52
                                                                                                                                                                                                                Local Similarity
                                                                                                                                    9
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application NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
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CTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGH-----
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Chen, Wensheng
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                          3.8%;
18.7%;
                                                                                                                                                                                  46;
                                                                                                                                                                               Score 77; DB 1
Pred. No. 1.2e4
46; Mismatches
                                                                                                                                                                                                             DB 10;
1.2e+02;
                                                                                                                                                                                                                                Length 1706;
                                                                                                                                                                                  Indels 172;
                                                                                                                                                                             Gaps
                                                                                                                               51
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	213 DCCALDKYLLINULEYPTDLMAGQEAHYYKYADRSQLEYQCQLISITIKEPNSECVRPQCSE	ργ	
	194 - VHSCFVD	P 89	
	156 EILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAV 193	Db Db	
	96 FVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRY 155	Qy Db	
	52VYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGI 95	Qy da	
	9 CTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGH	Qy Db	
20;	Query Match 3.8%; Score 77; DB 9; Length 4563; Best Local Similarity 18.7%; Pred. No. 5.4e+02; Matches 81; Conservative 46; Mismatches 135; Indels 172; Gaps		
	FILE REFERENCE: 870759 CURRENT APPLICATION NUMBER: US/09/870,759 CURRENT FILING DATE: 2002-01-14 PRIOR APPLICATION NUMBER: US 60/208,128 PRIOR FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 166 SOFTWARE: Patentin version 3.1 SEQ ID NO 128 SEQ ID NO 128 TYPE: PRT ORGANISM: Homo sapiens	us.	
DISEASE	RESULT 21 US-09-870-759-128 : Sequence 128, Application US/09870759 : Patent No. US20020177551A1 : GENERAL INFORMATION: : APPLICANT: TERMAN, David S : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC	RE US	
	308 IDVRTDINTLEISD 321	Qy Db	
	273 POGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENI 307	Оу	
	213 DGCALDKYLLNNLEYPTDLMAGOEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSE 272	Qy Db	
	194 -VHSCFVD	Оу	
	156 EILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAV 193	Qy Db	
	96 FYTTTVVISFHPLFVTKYDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRY 155 	Db Db	
	305 GSAYQAMILGVDSKNIFNFKVSQEGLKLSNDMMGSYAEMKFDHINSLNIAGL 356	DЬ	

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RESULT 23
US-09-738-626-4782
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US-09-802-640-32
  Sequence 4782, Application US/09738626 Publication No. US20020197605A1
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LENGTH: 4563
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GENES AND POLYMORPHISMS TITLE OF INVENTION: CARDIOVASCULAR DISEASE FILE REFERENCE: 24736-2048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kleyn Patrick
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                                                                                                                                                                                                             1977
                                                                                                                           2037 ID-----ALEMRD 2044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1711 GSAYQAMILGVDSKNIFNFKVSQEGLKLSNDMMGSYA---EMKFD-----HTNSLNIAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1662 CSLLV------LENELNAELGLSGASMKLTTNGRFREHNAKFSLDGKAALTELSL
                                                                                                                                                                                                                                                                                        1924 TGQLYSKFLLK-----AEPLAFTFSHDYKGSTSHHLVSRKSISAALEHKVSALLTP--AE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1804 NALDLTNNGKLRLEPLKLHVAGNLKGAYQNNEIKHIYAISSAALSASYKADTVAKVQGVE 1863
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                                                                                                                                                                                                                                                   273 PQGFGAVKTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 -----VYVKGLYD----QEGCR--NDEGGRQVAGISLPFDSCNVARTRSLNPRGI
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                                                                                                                                                                 IDVRTDINTLEISD 321
                                                                                                                                                                                                         QTGTWKLKTQFNNNEYSQDLDAYNTKDKIGVELTGRTLADLTLLDSPIKVPLLLSEPINI
                                                                                                                                                                                                                                                                                                                              DGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSE 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 77; DB 9;
18.7%; Pred. No. 5.4e+02;
ative 46; Mismatches 135
                                                                                                                                                                                                                                               ----GAAAKPAAAAQLRLLKK-----RSAEPENI 307
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Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 4782
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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APPLICANT:
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGP---TGQPVQFAIIGQPVY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 EFVILSD-TIGASMQTIAVNNEAYEDATEATVFGPFFVDDAPLVQNGDDIAFGAVGQPAW
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US20020160384A1
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38; Conservative
                                                                                                                                                                                                                                                                                                                            Ashkenazi, Avi J.
Baker, Kevin P.
                                                                                                 Gurney, Austin L.
                                                                                                                    Grimaldi, J. Christopher
                                                                                                                                                                                Gerber, Hanspeter
Gerritsen, Mary E.
                                                       Napier, Mary A.
                                                                          Kljavin, Ivar J.
                                                                                                                                       Godowski, Paul J.
                                                                                                                                                               Goddard, Audrey
                                                                                                                                                                                                                        Fong, Sherman
                                                                                                                                                                                                                                               Ferrara, Napoleone
                                                                                                                                                                                                                                                                  Eaton, Dan L.
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                   Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YOKOI,
Margaret Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-1
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OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/065770
OR PILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/0877106
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OR APPLICATION NUMBER: 60/087607
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OR APPLICATION NUMBER: 60/087827
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OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088025
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/049787
FILING DATE: 1997-06-16
APPLICATION NUMBER: 60/062250
APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60 FILING DATE: 1998-06-1 APPLICATION NUMBER: 60 FILING DATE: 1998-06-1
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APPLICATION NUMBER: 60
FILING DATE: 1998-06-1
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                                                                                                               NUMBER: 60/
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                 DR FILING DATE: 1998-06-24

PR APPLICATION NUMBER: 60/090535

PR FILING DATE: 1998-06-24

PR APPLICATION NUMBER: 60/090540

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PR APPLICATION NUMBER: 60/090542

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OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089801
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OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
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OR APPLICATION NUMBER: 60/090246
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OR APPLICATION NUMBER: 60/090349
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R APPLICATION NUMBER: 60/01
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R FILING DATE: 1998-06-
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FILING DATE: 1998-06-17
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DR APPLICATION NUMBER: 60/088824
DR FILING DATE: 1998-06-10
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DR APPLICATION NUMBER: 60/088861
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DR APPLICATION NUMBER: 60/088876
DR FILING DATE: 1998-06-11
DR APPLICATION NUMBER: 60/088876
DR FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 60/089532 6-17 60/089538 60/089440 60/089105

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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
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OR APPLICATION NUMBER: 60/05
OR FILING DATE: 1998-06-25
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/1
FILING DATE: 1998-06-25
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                            Ashkenazi, Avi J.
Baker, Kevin P.
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Pred. No. 77;
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APPLICANT: Zhang, Zemin

ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

ITITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: U5/09/989, 293A

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR APPLICATION NUMBER: 60/04978

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/06570

PRIOR FILING DATE: 1997-11-13

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PRIOR ETLING DATE: 1998-03-20
PRIOR EPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08322
PRIOR FILING DATE: 1998-04-28
PRIOR EPLICATION NUMBER: 60/084600
PRIOR PPLICATION NUMBER: 60/087106
PRIOR PPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-04
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Roy, Margaret Ann
Stewart, Timothy
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Pan, James
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DATE: 1998-07-09
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DR FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17

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60/088826 60/088824 60/088810 60/088742

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APPLICANN: WOOG, William I.
APPLICANN: MOOG, William I.
APPLICANN: Clang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: U5/09/989,735
CURRENT FILING DATE: 1907-10-17
PRIOR FILING DATE: 1907-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06571
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/06571
PRIOR APPLICATION NUMBER: 60/07594
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PRILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/08322
PRIOR APPLICATION NUMBER: 60/08707
PRIOR PRILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/08707
PRIOR PRILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/08702
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Godowski, Paul J.
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/092182
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
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Best Local Similarity
                                                                                                                                          TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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OR APPLICATION NUMBER: 60/062250
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OR APPLICATION NUMBER: 60/065186
OR FILING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/065311
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OR APPLICATION NUMBER: 60/066770
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Stewart, Timothy A.
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087827
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                                                    APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16
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OR APPLICATION NUMBER: 60/090557

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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091626
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978
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OR APPLICATION NUMBER: 60/092182
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T: Zhang, Zemin
INVENTION: Secreted and Tra
INVENTION: Acids Encoding
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                                            Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                             Tumas,
                                                                                                                                                                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                             Fong, Sherman
Gerber, Hanspeter
                                                                                                        Stewart,
                                                                                                                           Roy,
                                                                                                                                        Paoni, Nicholas F.
                                                                                                                                                         Pan,James
                                                                                                                                                                     Napier, Mary A.
                                                                                                                                                                                    Kljavin, Ivar
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                                                                                                                                                                                                                                                                                                                             Eaton, Dan L.
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art, Timothy A.
                                                                                            Daniel
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Pred. No. 77;
               Transmembrane Polypeptides and Nucleic
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CURRENT APPLICATION NUMBER: 05/08/2014 CURRENT EILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/065186 PRIOR APPLICATION NUMBER: 60/065186 PRIOR APPLICATION NUMBER: 60/065181 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/06570 PRIOR APPLICATION NUMBER: 60/075945 PRIOR APPLICATION NUMBER: 60/084600 PRIOR FILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/08707 PRIOR APPLICATION NUMBER: 60/087007 PRIOR APPLICATION NUMBER: 60/08707 PRIOR APPLICATION NUMBER: 60/08707 PRIOR APPLICATION NUMBER: 60/088021 PRIOR APPLICATION NUMBER: 60/088021 PRIOR APPLICATION NUMBER: 60/088023 PRIOR APPLICATION NUMBER: 60/088220 PRIOR APPLICATION NUMBER: 60/088220 PRIOR APPLICATION NUMBER: 60/088220 PRIOR APPLICATION NUMBER: 60/088220 PRIOR APPLICATION NUMBER: 60/088221 PRIOR APPLICATION NUMBER: 60/088221 PRIOR APPLICATION NUMBER: 60/088221 PRIOR APPLICATION NUMBER: 60/088222 PRIOR APPLICATION	REF
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Baker, Kevin P.
             Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
                                                              Gerritsen, Mary E.
Gurney, Austin
                                                                                                Fong, Sherman
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                                                                                                                 Ferrara, Napoleone
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                                                                       RRTD---HEDPRVKKTA-----FQISMAKPRPNS-----AEESNGPIYAFENLRAC
                                                                                                          -PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA
                                                                                                                                                                                                                           SERF-----LPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACV-----
                                                                                                                                                  -PAF----CDDQSPDAYSAYVLASLA----GEELQAVESSPKFNPNAIGVPQPYLNKLNY
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21.2%; Pred. No. 77;
tive 47; Mismatches
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FILING DATE: 1998-06-APPLICATION NUMBER: 60 FILING DATE: 1998-06-

60/089512 60/089440

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APPLICATION NUMBER: FILING DATE: 1998-06PRIOR PRIOR

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60/088876 60/088861 60/088858 FILING DATE: 1998-0 APPLICATION NUMBER:

1998-06-10

60/088824 60/088810 60/088742

60/088826

APPLICATION NUMBER:

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1998-06-10 1998-06-1

NUMBER:

1998-06-10

FILING DATE: 1998-06-10

APPLICATION NUMBER:

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US-09-993-687-124
; Sequence 124, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:

PRIOR PRIOR

APPLICATION NUMBER: 60/

FILING DATE: 1998-06-24

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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24

60/090535 60/090472 60/090445 60/090444 60/090435

PRIOR PRIOR

FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 6
FILING DATE: 1998-06-APPLICATION NUMBER: 60/ FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-23

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1998-06-1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-18

60/089947 806680/09 60/089907 60/089801 60/089653 60/089600

60/089952

APPLICATION NUMBER: 60/

APPLICATION NUMBER: FILING DATE: 1998-06-17

FILING DATE: 1998-06-1

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/

APPLICATION NUMBER:

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CURRENT APPLICATION NUMBER: US/09/93,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
FILE REFERENCE: P2730P1C11
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OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
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OR APPLICATION NUMBER: 60/087759
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OR APPLICATION NUMBER: 60/087759
OR APPLICATION NUMBER: 60/087827
OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/088021
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OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-03-20
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FILING DATE: 1998-04-28
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Baker, Kevin P.
Botstein, David
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Kljavin, Ivar J.
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Godowski, Paul J.
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Eaton, Dan L.
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OR APPLICATION NUMBER: 60/089801
OR FILING DATE: 1998-06-18
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OR APPLICATION NUMBER: 60/089908
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OR APPLICATION NUMBER: 60/089947
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OR APPLICATION NUMBER: 60/089948
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OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/08810
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088824
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R APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088212
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-PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA 284
                                                                                                                               VQCFYMEADKTVSAQIE----VSEITTAFQTQIVPMPVC--RYEILDGGPTGQPVQFAIIG
                               -PAF----CDDQSPDAYSAYVLASLA----GEELQAVESSPKFNPNAIGVPQPYLNKLNY
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PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1997-66-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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CURRENT FILING DATE: 2001-11-19
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Williams, P. Mickey
Wood, William I.
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OR APPLICATION NUMBER: 60/088212
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OR APPLICATION NUMBER: 60/088217
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OR APPLICATION NUMBER: 60/088734
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DR APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
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APPLICATION UMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/090542
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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                                YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYV------KGLYDQEGCRNDE 67
                                                                       l Similarity
72; Conser
                                                                       Conservative
                                                                                                                                                NUMBER: 60/092182
: 1998-07-09
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                                                                       47;
                                                                     Score 76.5; D
Pred. No. 77;
47; Mismatches
                                                                                                         DB 9;
                                                                       123;
                                                                                                         Length 1184;
                                                                       Indels
                                                                       97;
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APPLICATION NUMBER: 60/088858
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876

R FILING DATE: 1998-06
R APPLICATION NUMBER:
R FILING DATE: 1998-06
R FILING DATE: 1998-06

NUMBER: 60/089948 1998-06-19 1998-06-19 1998-06-18 1998-06-18

R APPLICATION NUMBER:
R FILING DATE: 1998-06
R APPLICATION NUMBER:
R FILING DATE: 1998-06
R APPLICATION NUMBER:

APPLICATION NUMBER:

60/089947 806680/09 60/089907

Gaps

19;

60/089598

NUMBER: 60/089538 1998-06-17

APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538

APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-16

FILING DATE: 1998-06-1 APPLICATION NUMBER: 60 FILING DATE: 1998-06-1

60/089105

60/089440 60/089512

1998-06-11

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17

APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

NUMBER: 60/089801 1998-06-18

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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
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PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05963
PRIOR FILING DATE: 1997-09-17
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TITLE OF INVENTION:
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OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/05
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OR APPLICATION NUMBER: 60/05
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                                                                                                                                                                                               FILING DATE: 1997-U9-16
(APPLICATION NUMBER: 60/059352
CAPPLICATION NUMBER: 60/059352
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumas, Daniel
Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gao, Wei-Qiang
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beresini, Maureen
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5. US20030004311A1
                                                 NUMBER: 60/062250
: 1997-10-17
        NUMBER: 60/062285: 1997-10-17
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                                                                                                                                     60/059836
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OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063733
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063738
OR FILING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063755
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OR APPLICATION NUMBER: 60/072320
OR FILING DATE: 1998-01-23
OR APPLICATION NUMBER: 60/073612
OR FILING DATE: 1998-02-04
OR APPLICATION NUMBER: 60/074086
OR FILING DATE: 1998-02-09
OR APPLICATION NUMBER: 60/074092
OR FILING DATE: 1998-02-09
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                                                                                                  FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/APPLICATION NUMBER: 6
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APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065846
FILING DATE: 1997-11-17
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APPLICATION NUMBER: 60/063127
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063327
FILING DATE: 1997-10-27
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APPLICATION NUMBER:
                        APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27
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FILING DATE: 1997-10-24
                                                                               FILING DATE: 1998-02-27
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OR APPLICATION NUMBER: 60/089532
OR FILLING DATE: 1998-06-17
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FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-05-15
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-05-22
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/
FILING DATE: 1998-04-29
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FILING DATE: 1998-05-22
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           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730p1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/065186
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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                                                                                                                                                                    Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                      Tumas,
                                                                                                                                                                                                                                                                                                                Gurney,Austin L
Kljavin,Ivar J.
                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, J.Christopher
                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen, Mary
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                                                                                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                    Paoni,Nicholas F.
                                                                                                                                                                                                                                                                                 Pan,James
                                                                                                                                                                                                                                                                                               Napier, Mary A.
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47; Mismatches
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PRIOR PRIOR

APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759

APPLICATION NUMBER:
APPLICATION NUMBER:

1998-04-28

60/084600

60/083322

FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/0 FILING DATE: 1998-05-28

60/087106

APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25 APPLICATION NUMBER: 60/078910

FILING DATE: 1998-03-20

FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/ FILING DATE: 1997-11-24

60/066770 60/065311

FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/0

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R APPLICATION NUMBER: 60/08
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R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08
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R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/08
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R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-16
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FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/0
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R FILING DATE: 1998-06
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R APPLICATION NUMBER: 60/08
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R PAPPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08

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PR APPLICATION NUMBEE: 60/991478

DR FILING DATE: 1998-07-02

PR APPLICATION NUMBER: 60/091544

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091519

DR APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PAF----CDDQSPDAYSAYVLASLA----GEELQAVESSPKFNPNAIGVPQPYLNKLNY
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                                                                                                                                                                                                                                                                             Ashkenazi, Avi J.
Baker, Kevin P.
           Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                         Gurney, Austin L. Kljavin, Ivar J.
                                                                                                                      Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                   Goddard, Audrey
                                                                                                                                                                                 Gerber, Hanspeter
 Tumas,
                                                             Pan, James
                                                                         Napier, Mary A.
                                                                                                                                                                   Gerritsen, Mary E.
                                                                                                                                                                                                    Fong, Sherman
                                                                                                                                                                                                                 Eaton, Dan L.
Ferrara, Napoleone
                                                                                                                                                                                                                                               Desnoyers, Luc
                                                                                                                                                                                                                                                              Botstein, David
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Daniel
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21.2%;
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Pred. No. 77;
47; Mismatches 123;
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FRIOR APPLICATION NUMBER: US/09/99.

PRIOR APPLICATION NUMBER: 60/049787

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
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OR FILING DATE: 1998-04-28
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OR FILING DATE: 1997-10-17
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FILING DATE: 1998-06-04
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APPLICATION N
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/088030
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FILING DATE: 1998-06-03
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OR FILING DATE: 1998-06-24
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OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/090444
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OR APPLICATION NUMBER: 60/090472
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090535
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OR APPLICATION NUMBER: 60/08944
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OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089514
OR APPLICATION NUMBER: 60/089514
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OR APPLICATION NUMBER: 60/089600
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OR APPLICATION NUMBER: 60/089601
OR APPLICATION NUMBER: 60/089601
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60
FILING DATE: 1998-06-1
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RESULT 36 US-10-121-049-412

Sequence 412, A Publication No.

Application US/10121049

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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maur.
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc

Beresini, Maureen

DeForge, Laura Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang Gerritsen, Mary

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R FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/
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EEAPPSAAHFRFYQ------IEGDRYDYNTVPFNEDD
                                                                         -PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA
                                                                                                   -PAF----CDDQSPDAYSAYVLASLA----GEELQAVESSPKFNPNAIGVPQPYLNKLNY
                                                   RRTD---
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                                                   HEDPRVKKTA-----FQISMAKPRPNS----AEESNGPIYAFENLRAC
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21.2%; Pred. No. 77;
Live 47; Mismatches
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US-10-123-904-412; Sequence 412, Application US/10123904; Publication No. US20030022328A1
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SEQ ID NO 412
LENGTH: 1184
TYPE: PRT
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CURRENT FILING DATE: 2002-04-12
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Tumas, Daniel
Watanabe, Colin K
Wood, William
                                                                 Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
                                             Stewart, Timothy A.
                                                                                                                                Goddard, Audrey
                                                                                                                                                Gerritsen, Mary E.
                                                                                                                                                                Gao, Wei-Qiang
                                                                                                                                                                               Desnoyers, Luc
Filvaroff, Ellen
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Wood, William
                                                                                                                  Godowski,Paul J.
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Pred. No. 77;
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US-10-140-470-412; Sequence 412, Apr
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Prior Application removed -
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 412
LENGTH: 1184
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NOS: 550
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                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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APPLICANT:
APPLICANT:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 YSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYV------KGLYDQEGCRNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEIL-----NADGCALDKYLLNNLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQCFYMEADKTVSAQIE---VSEITTAFQTQIVPMPVC--RYEILDGGPTGQPVQFAIIG
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                                                                                                                                                                                                                                                                    Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                             Zhang, Zemin
                                                                                                                                                                               Wood, William
                                                                                                                                                                                              Tumas, Daniel
Watanabe, Colin K
                                                                                                                                                                                                                                 Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                             Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                             Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                       Smith, Victoria
                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                  DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                   Beresini,Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10140470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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21.2%; Pred. No. 77;
tive 47; Mismatches
                                                   See Palm or File Wrapper
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                                                                                                                                              AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
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RESULT 39
US-09-990-438-124
Sequence 124, Application US/09990438
Publication No. US20030027754A1
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US-10-140-470-412
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Best Local
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               CURRENT APPLICATION NUMBER: US/09/990,438
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-017
                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P.
                                                                                                                                               TITLE OF INVENTION: Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PlC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 72; Conserv
APPLICATION NUMBER: 60/
FILING DATE: 1997-11-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PAF----CDDQSPDAYSAYVLASLA----GEELQAVESSPKENPNAIGVPQPYLNKLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEIL-----NADGCALDKYLLNNLEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQRR-----NKREDRT-----FLVGNLEIRERRLFNLDVPESRRCFVKVRAYR 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVD-----RAYR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSVDFRDEVTSEP-LNAGKYKVHLD-STQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFE 717
                                                                                                                                                                                                     Zhang,
                                                                                                                                                                                                                                      Watanabe, Colin K. Williams, P. Mickey
                                                                                                                                                                                                                                                                                               Stewart,
                                                                                                                                                                                                                                                                                                                Paoni, Nicholas F. Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                           Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker, Kevin P. Botstein, David
                                                                                                                                                                                                                         Wood, William
                                                                                                                                                                                                                                                                                                                                                                                            Kljavin, Ivar
                                                                                                                                                                                                                                                                                                                                                                                                                             Grimaldi, J.Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                       Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACV-----
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                                                                                                                                                                                                       Zemin
                                                                                                                                                                                                                                                                           Daniel
                                                                                                                                                                                                                                                                                             Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 76.5;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                    and
                                                                                                                                                                                    Nucleic
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-09
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
               APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16
                                                  APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-16
                                                                                                                                                                              APPLICATION NUMBER:
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FILING DATE: 1998-06-11
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                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
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FILING DATE: 1997-11-24
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                                                                                                        APPLICATION NUMBER: 60/089105
                                                                                                                            FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60,
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OR APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/091544
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72; Conserv
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Baker, Kevin P.
                   Stewart, in Daniel
Watanabe, Colin K. Williams, P. Mickey
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                                                                                                                                                               Godowski, Paul
                                                                                                                                                                          Gerritsen, Mary
Goddard, Audrey
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                                                          Roy, Margaret Ann
                                                                        Paoni, Nicholas F
                                                                                                   Napier, Mary A.
                                                                                                                     Kljavin,Ivar J.
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Pred. No. 77;
47; Mismatches
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CURRENT APPLICATION NUMBER: (05/09/990,562
CURRENT ETLING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/06276
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/08332
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E OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-11
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                  NUMBER: 60/090678
1998-06-25
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091626
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091978
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.8%; Score 76.5; DB 9; Best Local Similarity 21.2%; Pred. No. 77; Matches 72; Conservative 47; Mismatches 123;
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PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
903 EEAPPSAAHFRFYQ-----IEGDRYDYNTVPFNEDD 933
                                              285 AAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDN 323
                                                                                                           960
                                                                                                                                     228 - PTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQG--FGAVKTGGA 284
                                                                                                                                                                                                                                        174 OPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEIL-----NADGCALDKYLLNNLEY 227
                                                                                                                                                                                                                                                                                      718 NORR------NKREDRT-----FLVGNLEIRERRLFNLDVPESRRCFVKVRAYR 760
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                                                                                            RRTD---HEDPRYKKTA-----FQISMAKPRPNS-----AEESNGPIYAFENLRAC 902
                                                                                                                                                                                          -PAF----CDDQSPDAYSAYVLASLA----GEELQAVESSPKFNPNAIGVPQPYLNKLNY
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APPLICATION NUMBER: 60/090694
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19;

Search completed: March 24, 2003, 08:55:45 Job time: 39 secs

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A49772

A49772

cuticle protein cut-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 01-I
C;Accession: A49772; S27799
R;Sebastiano, M.; Lassandroo, F.; Bazzicalupo, P.
Dev. Biol. 146, 519-530, 1991
A;Title: cut-1 a Caenorhabditis elegans gene coding for a dauer-special field of the compared with conceptual translation
A;Reference number: A49772; MUID:91323673; PMID:1864469
A;Accession: A49772
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-423 <SEBS
A;Cross-references: GB:M55997
R;Sebastiano, M.; Lassandro, F.; Bazzicalupo, P.
submitted to the EMBL Data Library, July 1991
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Datte: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_
C;Accession: T21239
R;Sims, M.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19395
A;Reference number: Z19395
A;Accession: T2139
A;Acc
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Caenorhabditis elegans hypothetical protein F22B5.3
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Pred. No. 9.4e-114;
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A; Gene: CUT-1
A; Introns: 360/
C; Superfamily:
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                                                                                                                                                                     A;Gene: CESP:F53F1.1
A;Map position: 5
A;Introns: 57/1; 136
                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library
A;Reference number: Z19583
A;Accession: T22563
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
T22563
hypothetical protein F53F1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T22563
R;Burton, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: CUT-1 a Caenorhabditis elegans gene coding A;Reference number: S27799
A;Recession: S27799
A;Molecule type: DNA
A;Residues: 'R',77-78,'YP',121-423 <SE2>
A;Cross references: EMBL:M55997; NID:g156271; PID:g156272
C;Genetics: '
 S
                                                                                                                                                                                                                      A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z81088; PIDN:CAB03124.1; GSPDB:GN00023; CESP:F53F1.1 A;Experimental source: clone F53F1
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A; Residues: 1-364 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRSQ
|||||||||||||
DTFCAVVHSCTVDDGNGDTVQILNEEGCALDKFLLNNLEYPTDLMAGQEAHVYKYADRSQ
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                                 VPIQNSLYGDVQVECDSRTISVQIKTEKPFVGVIFVKDFASEEVCTSRGTGRLSAFLEIE
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FDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSE 138
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                                                                                                                                                                     57/1; 136/3;
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273; Conserv
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65.8%;
                                                                                             35.8%; Score 725.5; DB 2;
47.6%; Pred. No. 5.7e-56;
tive 51; Mismatches 84;
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Pred. No. 2
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2.2e-113;
nes 67;
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Maximum Match 100%
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                               DB seq length: 0
DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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A;Map position: 2 A;Introns: 40/1; 115/2; 361/3 C;Superfamily: Caenorhabditis elegans hypothetical protein F22B5.3

A;Cross-references: EMBL:Z49125; PIDN:CAA88934.1; GSPDB:GN00020; CESP:C47G2.1 A;Experimental source: clone C47G2 C;Genetics: C;Genetics: A;Gene: CESP:C47G2.1

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-424 <WIL>

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	2 T14850	ō	109	4.4	88.5	5
	2 A41519	is 	251	4.4	90	44
	2 T30581	7	119	4.4	90	43
	2 S48944	ō 	108	4.4	90	42
	2 A40970	<u>س</u> 	84	4.4	90	41
	2 T22486	<u>-</u>	74	4.4	90	40
	2 T11616	4	224	4.5	92	39
	2 T38883	<u>ت</u>	649	4.6	93.5	38
	2 T42233	٠	158	4.7	94.5	37
	1 URXLA2	ű	87	4.7	94.5	36
	2 \$17855	<del>ن</del>	93	4.9	100	35
	2 T22367		80	5.0	101.5	34
	2 A83394	9	27	5.0	102	33
	2 в89614	ŭ	49	5. 3	108	32
	2 T19902	<u>.</u>	446	5 3	108	31
	2 T19553	2	94	٠. ن	T10.5	30

## ALIGNMENTS

RESULT 1
T20032
Typothetical protein C47G2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sate: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000
C;Accession: T20032
R;Palmer, S.
Submitted to the EMBL Data Library, April 1995
A.Reference number: Z19213

Indels Length

15;

Gaps

7;

466

406 199 346

286

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hypothetical protein M142.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T23760 R;MCMurray, A. submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z49207; PIDN:CAA89068.1; A;Experimental source: clone R07E3 C;Genetics: A;Gene: CESP:R07E3.3 A;Map position: X A;Introns: 2/3; 50/2; 88/3; 127/2; 180/3; 214/1; 2
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A; Reference number: Z19832
A; Accession: T24028
A; Status: preliminary; translated
A; Molecule type: DNA
A; Residues: 1-290 <WIL>
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R;Cottage, A.
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42.2%; Pred. No. 4.2e-49;
7ative 50; Mismatches 79
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A; Nolecule type: DNA
A; Residues: 1-484 <WIL>
A; Residues: 1-484 <WIL>
A; Cross-references: EMBL: 266496; PIDN: CAA91280.1; GSPDB: GN00020;
A; Cross-references: Clone E04D5
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                       A; Introns: 14/1; 92/3; 139/2; 253/3; 338/1; 445/1
                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                               A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 11/3; 39/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:M142.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: Z73428; PIDN: CAA97806.1; GSPDB: GN00021; CESP: M142.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-550 <WIL>
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                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                               CESP: E04D5.3
                                       TRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQ 146
                                                                                                               GEPEIECGPTSITINFNTRNAFEGHYYYKGLYDQEGCRNDEGGRQVAGISLPFDSCNVAR 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-EPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTD-INT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FREQIYQMPQCAYTLRKGAPDGPIVRPATLGESVYHRWECIEVEGADKDTFGMLVHSCYV
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                                                                                          GEPEVVCETASISLLFKTRNSFNGKVFVKGYVSEPSCMTVGDGKTGHRFEVRHDSCGVRR
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                                                                                                                                                                   al Similarity
113; Conserv
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                                                                                                                                                             47; Mismatches
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                                                                                                                                                                                Score 595; DB 2;
Pred. No. 2.6e-44;
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Length Indels

CESP: E04D5.3

6

Gaps

4;

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RESULT 8

T21141

T21141

T21141

hypothetical protein F20D1.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T21141
R;Burton, J.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19382
A;Accession: T21141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T21141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cacss-references: EMBL:Z78542; PIDN:CAB01742.1; GSPDB:GN00028; CESP:F20D1.8
A;Experimental source: clone F20D1
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Anap position: X
A;Introns: 32/3; 48/1; 80/2; 110/3; 158/2; 194/2; 245/1
submitted to the EMBL Data Library, November 1995 A;Reference number: Z19895 A;Recession: T24467 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-384 <WIL> A;Cross-references: EMBL:Z66565; PIDN:CAA91480.1; G:A;Experimental source: clone T04F8
                                                                                                                                                                                                                                 RESULT 9
T24467
                                                                                                                                                          hypothetical protein T04F8.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: T-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T24467
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113;
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40.2%; Pred. No. 4.1
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              PIDN:CAA91480.1; GSPDB:GNÖ0028; CESP:T04F8.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F53B6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                A; Gene: CESP:F53B6.6
                                                                                                                                                                                                                                                                                                                A; Experimental source:
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                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-610 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, A; Reference number: Z19578
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A;Introns: 16/3; 55/1; 99/3; 147/2; 195/1; 221/2; 276/3; 292/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F22
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A; Gene: CESP:T04F8.4
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 -----NDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LIAFCTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                               ß
DEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYME 125
                                                                                                                                TTLIALSYS--IPVDNGVEGEPEIECGPTSITINENTRNAFEGHVYVKGLYDQEGC--RN
                                                                                                              TILILLSTSSCFEIQNGVVGKPEVFCGIDTIRVKVNTEHPFNGRIYVDGESDKQHCVQHS 120
                                                ADAHSSPQEFTIPIGACNMRRQRTLHPRGISFSFTMITSFHPFFVTGMDRAFSIRCFFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLKKRSAEPENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDL-MAGQEAH
                                                                                                                                                                                  101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKLLVVAVTFFTF1FVLFVTT1LVVVYHRYCKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P----FGFSMFMGLSIALIAAVIITISFKFRPNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFKPKDAD---MFSQTVYVMDKENGDSTSAQAAEIRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYKYADRSQLFYQCQISITIKEPNSEC---VRPQCSEPQGFGAVKTGGAAAKPAAAAQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQCDSE----DYGLLVHSCYVEDGQGEKQMIIDERGCHTDRLLLGDPTYVEALNMAYRESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCMYKEAARTVTAAIDVSNLPTESVQSDLPMPTCSYTIRRDQLDGPILKYAKVGDQVVHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFKFADRIAVRFQCEIRLCLKD-DGGCDGITPPMCS-----FKDANSNEKQIVKRNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVEFTYFVLGFSAAIQDDNELIGQPEIQCNADTIDMQFRTRKQFNGKVYVKGSYNRPECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                               25.28; ilarity 37.48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                              EMBL:Z81086; PIDN:CAB03116.1; GSPDB:GN00019; CESP:F53B6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.0%;
                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                            Score 511; DB 2;
Pred. No. 8.9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 546.5; DB 2
Pred. No. 3.5e-40;
                                                                                                                                                                               Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                            October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155;
                                                                                                                                                                                                                                             532/2; 546/1
                                                                                                                                                                                                          Length 610
                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F22B5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LDPQTICLA
                                                                                                                                                                               10;
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                                                                                                                                                                             Gaps
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RESULT 11
T24323
hypothetical protein ZK265.8 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C; Accession: T24323; T27813
R; Lennard, N.
submitted to the EMBL Data Library, July 1996
***Bafarence number: Z19874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1996
A; Reference number: Z20422
A; Recession: T27813
A; Kotatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-440 <MIZ>
A; Cross references: EMBL: Z81143; PIDN: CAB03520.1; GSPDB: GN00019; CESP: ZK265.8
A; Experimental Source: clone ZK265
C; Genetics:
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A;Map position: 1
A;Introns: 12/3; 51/1; 93/3; 197/1; 278/3; 353/2; 357/2; 391/3;
hypothetical protein W01A8.3 - Ca
C; Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-440 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                  285 AAKPAAAAQLRLLKKRSAEP 304
                                                                                                                                                                                                                                                                                                   124 KCFFEEANKGLTAELGVSMIPTTELEARHGIPGCTYSIHRSTIDELDAGRPAGNVIQFAR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 KVQLYFTCTVQLCYKH-DGGCEGITPPQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 33.4 es 107; Conservative
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                                                                                                                                                                   QRAYAESSVFKFADKPGVWFFCQVQMCMKK-HGMCDGITPPSCGSMSRVISVGGEDNGGF
                                                                                                                                                                                                 M-AGQEAHVYKYADRSQLFYQCQISITIKEPNSEC---VRPQC---SEPQGFGAVKTGGA 284
                                                                                                                                                                                                                                  VGERVLHQWHCNDQ---MYGVLINNCYVTDGFGKKADVIDDKGCPIDPILITGIRYSSDL
                                                                                                                                                                                                                                                         IGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDL
                                                                                                                                                                                                                                                                                                                      QCFYMBADKTVSAQIEVSEITTAFQTQIVPMPVCRYBI-----LDGG-PTGQPVQFAI 171
                                                                                                                                                                                                                                                                                                                                                                     CRNDEGGRQVA---GISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                       LKILIIAWTGWRVANAISIDNEIIGEPDIECLEDEIRIWVKTRKIFAGRIYAKGRAELED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.6%;
                                                                                                   316
                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 477.5; DE Pred. No. 5e-34; 56; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
                                                                                                               Query Match
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hes 113;
                 3
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                                                                                                 Local
                                         PEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGR----QVAGISLPF-DSCNV
               PKLECGSEGIRLHINPTGTFGGHVYVRGFFPQTVCHLNYCTRLTNRPIVMDLPFRGPCNV
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submitted to the EMBL Data Library, April 1995
A;Reference number: Z19983
A;Accession: T25120
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T22C8.7 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T25120
                                                                                                                                                          A; Map position: 2
A; Introns: 36/3; 66/2;
                                                                                                                                                                                                             A; Gene: CESP:T22C8.7
                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Restdues: 1-609 <WIL>
A;Cross-references: EMBL:Z49071; PIDN:CAA888879.1; GSPDB:GN00020; CESP:T22C8.7
A;Experimental source: clone T22C8
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A;Experimental source: clone W01A8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 PEIECGPTSITINFNTRNAFEGHYYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CESP:W01A8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVMPKCEYSVRRDGPNGPTLTYANVGDIVFHVWEC---TPADMGMLVKKCFVTDGDGEDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIALIAAVIITIS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVRPQC-----SEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVVDFDGCATDPFLLSELSYDASLMRAHASSQVFKYADSNQLYFTCQIRLCQKQMGMCQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EILNADGCALDKYLLNNLEYPTDLM-AGQEAHVYKYADRSQLFYQCQISITIKEPN--SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANPRGVNFMVTVIVSFHPAGFITKNDRAFHVKCFYMEPDEIVTQNIDVSMIPTTELSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTPPNCGVKKLLSEASGDG:
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                                                  Similarity 38.:
99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                          98/3; 146/2; 219/2; 274/3; 399/3; 475/1; 576/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%; Score 476; DB 2; 31.4%; Pred. No. 5.7e-34
                                                                         22.3%; Score 451; DB 2; 38.2%; Pred. No. 1.7e-31;
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                                                     Mismatches
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                                                     107;
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                                                                                                     Length 609
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84
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hypothetical protein y53c12B.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27131
R;Kershaw, J.; Lennard, N.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z20316
A;Accession: T27131
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:Z99278; PIDN:CAB16488.1; GSPDB:GN00020; CESP:Y53C12B.6
A;Cross-references: EMBL:Z99278; PIDN:CAB16488.1; GSPDB:GN00020; CESP:Y53C12B.6
A;Gene: CESP:Y53C12B.6
A;Map position: 2
A;Introns: 23/1; 87/3; 167/1; 205/3; 279/3
                                             RESULT 15
T34329
T34329
Appothetical protein K06Al.3 - Caenorhabditis elegans
C;Specites: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t
C:Accession: T34329
T-11 1995
                    R;Fulton, L. submitted to the EMBL Data Library, July 1995 abmitted to the sequence of C. elegans cos
A; Reference number: A; Accession: T34329
               A;Description: The sequence A;Reference number: Z21507
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                                                                                                                                                                                                                                                                                                                                  T-VDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLM-AGQEAHVYKYA
                                                                                                                                                                                                                                  DNHIVYFKCNIRITVKNPSGECPVNNCS-PNG
                                                                                                                                                                                                                                                                                                                                                                        APQPRILSDEPKLPTCDYRVEVTGGKAVAGGIVTSSLSETASQIANVGDSVIHIWTCSGD
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                                                                                                                                                                                                                                                                                                                                                                                                        EITTAFQTQIVPMPVCRYEI-LDGGP------TGQPVQFAIIGQPVYHKWTCDSE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                              FDDCPSRRKRQIVAPRGMTMSSVLVVSYHGSIITHRDVAYQIDCFYREENSRVETMLSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDSCNVARTRSL-NPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKDFQFIDERGCVTDFSLFPEVSYSDDLKSAFTAVRAFRYADQVMVHFSCQITTCQKQEN
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                                                                                              #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                              cosmid K06A1
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                                                                                                                                                                                                                           A; Map position: : A; Introns: 17/3;
                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein M28.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Coct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                          A; Gene: CESP: M28.1
                                                                                                                                                                                                                                                                                    A; Experimental source: clone M28
                                                                                                                                                                                                                                                                                                                                                             R;Gardoner, A.
submitted to the EMBL Data Library,
A;Reference number: Z19803
A;Accession: T23814
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A;Molecule type: DNA
A;Residues: 1-747 <FUL>
A;Cross-references: EMBL:U23449; PIDN:AAC24298.1; GSPDB:GN00020; CESP:K06Al.3
A;Experimental source: strain Bristol N2; clone K06Al
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A; Introns: 29/1; 62/3;
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                                                                                                                                                                     Matches
                                                                                                                                                                                               Query Match
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                    195
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                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IAFCTTLIALSYS----IPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CESP:K06A1.3
HSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQ-EAHVYKYADRSQLFYQCQ
                                                                                                                          ISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQI 134
                                            DVNMTDEQEINGTVEPPSCDYLISD--QNGNSVQNSLVGELVRHQWVCKGGLTNKLKMLV
                                                                     EVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNL
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                                                                                                                                                                     90;
                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                            37/1;
                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                      226/2; 275/3; 323/2; 453/3; 540/3; 574/1
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                                                                                                                                                                              19.4%;
29.7%;
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                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                Score 393; DB 2;
Pred. No. 2.4e-26;
56; Mismatches 127
                                                                                                                                                                                                                                                                                                PIDN:CAA90131.2; GSPDB:GN00020; CESP:M28.1
                                                                                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 409.5;
Pred. No. le
                                                                                                                                                                                                                                                                                                                                                                                          June
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                                                                                                                                                                                                                                                                                                                                               GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                          1995
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                                                                                                                                                                  127;
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                                                                                                                                                                                            Length 647;
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hypothetical protein W04C9.3 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tc C:Accession: T33556 R:Fulton, R.; Rohlfing, T.; Morris, M.
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A;Gene: w28.1
A;Map position: 2
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Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological platform for investigation for investigation for investigation for investigation for 
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A; Residues: 1-670 <STO>
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R; Fulton, R.; Rohlfing, T.; Morris, submitted to the EMBL Data Library,
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                                                                                                                           29-Oct-1999 #text_change
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C;Genetics:
A;Gene: CESP:F10E7.10
A;Gene: 41/3; 85/3; 266/3; 289/2; 328/2; 378/1
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A; Residues: 1-437 < PAU>
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                                                                                                                   121 CFYMEADKTVSAQIEVS-EITTAFQTQIVP-----MPVCRYEILDGGPTGQPVQFAIIG 173
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                                      CVY--ADSHVMKDIESTLDISEAPPLQLSPQFDAPVMPKCNYSIRKQGKDGPPVQYASIG
                                                                                                                                                                                                        MECVS----RNQNKIEVAHDKCGVVNEKTEQPNCSIRRLCIFVQLHPLFVTESDRSYCAQ 116
                                                                                                                                                                                                                                                   EGCRNDEGGRQVAGISLPEDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQ 120
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-477 < PUL>
A; Residues: 1-477 < PUL>
A; Cross-references: EMBL; AF098999; PIDN: AAC68726.1; GSPDB:GN00019; CESP:W04C9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 10/3; 47/2; 140/2; 217/2; 300/1; 332/1; 458/2
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cn 18.6%; Score 376.5; DB 2; Length 1 Similarity 27.9%; Pred. No. 4.4e-25; 79; Conservative 65. Microscited 18.6%; Conservative 65. Microscited 18.6%; DB 2; Length 18.6%; DB 2; DB
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232 MAGQEAHVYKYADRSQLFYQCQISITIKEPNSEC---VRPQCS 271 3 IRLIAFCTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEG 62 DRAYRVOCFYMEADKTVSAQIEVSEI-TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAII 172 CRRQFLAPNQAGG----SFTVRLGDCGMRRSRQISGHSPRGVNQHITFVANFHPNLATKE 116 GMTIVHRWDCD--TSGNYGILLRGCTILDSRGVESFPLLDENGCSVSRDFPQVVYLPSLT 234 GOPVYHKWTCDSETVDTFCAVVHSCFVDDGNG-DTVEILNADGCALDKYLLNNLEYPTDL ERSFNIRCFYAHSESVVKADLDVSSMPEESFEQGVTIVPQCTYSLREGTFEGPKVSNTRV 176 CR-----NDEGGRQVAGISLPFDSCNVARTRSL---NPRGIFVTTTVVISFHPLFVTKV 113 21; Gaps 60 231

hypothetical protein F10E7.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999 C;Accession: T34211 A; Cross-references: EMBL: U41264; PIDN: AAA82426.1; CESP: F10E7.10 Query Match 17.6%; Score 357.5; DB 2; Best Local Similarity 31.6%; Pred. No. 1.8e-23; Matches 87; Conservative 47; Mismatches 122; MMIRLIAFCTTLIALSYSIPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQ 60 F10E7 Indels Length 19; Gaps

174

7;

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A;Cross-references: EMBL:Z68318; PIDN:CAA92696.1; GSPDB:GN00020; A;Experimental source: clone T21B10 C;Genetics:
                                                                                                                                                                                                                                                                                hypothetical protein T21B10.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T25042 R;Baynes, C.
                                                        A; Introns: 40/2;
                                                                             A; Map position:
                                                                                            A; Gene: CESP:T21B10.6
                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-366 <WIL>
                                                                                                                                                                                                     A;Status: preliminary; translated from
                                                                                                                                                                                                                            A; Reference number: A; Accession: T25042
                                                                                                                                                                                                                                           submitted to the EMBL Data Library, December 1995 A; Reference number: Z19973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein B0511.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33114
R;Tin-Wollam, A.; Sutterer, C.; Ozersky, P.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid B0511.
A;Reference number: Z21285
A;Accession: T33114
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A; Residues: 1-225 <T
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                   Query Match
 Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGRVFVLGHSQDKDCVSRETGRRTTSITVPRDKCGVETVQHGKGAGYTSSVNIVISFHDK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENNKLSARVMSKAFRFGDDVAVEFECNVRLDLRNGTS-CPRPRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTD-LMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVHVNAPLEHVWTCDGTNLDLFCMTVHDCVINEGKSKRRSKIIDSEGCSLDTTRLPNLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLTKVDRAYNITCLYAPTGDVVSYALTVQPSLLKDIQVLAEQPSCEYEVFD-VRTRRPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFQETHVFKFAQRTVTRFICQIKICMK--GDDCKR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGQEAHVYKYADRSQLFYQCQISITIKEPNSECVR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70; Conservative
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                                        2; 53/3;
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                                                      76/2; 171/3; 259/2; 341/3
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 14.5%;
24.6%;
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Pred. No. 3.1e-22;
2; Mismatches 108;
 Score 293;
Pred. No.
                                                                                                                                                                                                        GB/EMBL/DDBC
6.7e-18;
               Length
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                   366;
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A;Residues: 1-344 <WIL>
A;Cross-references: EMBL:282073; PIDN:CAB04922.1; GSPDB:GN00023; CESP:W06D12.1
A;Experimental source: clone W06D12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein W06D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T26728 R;Basham, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T26228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z20177
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 251
                                    330
                                                                       191
                                                                                                          303
                                                                                                                                           140
                                                                                                                                                                             262
                                                                                                                                                                                                                                              211 NADGCALDKYLLNNLEY-PTDLMAGQEAHVYKYADRSQLFYQCQISITIKE------P 261
                                                                                                                                                                                                                                                                                                                   151 PVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEIL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320
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LPESEV----GNPTGNRKFHVPTNASNDVCFTRTN----LILSLLILAALGIVTISLMY
                             LRHRALLQHNGQPV-----ILAAVQNGICMSPFGFSMFMGLSIALIAAV-IITISFKF 381
                                                                   TSNSDYSADFLDDELEDEVDKMSRIPSVTMNRLIRRDVAGGNTKLLADVDVAAPSVNVQD
                                                                                                                                       TEVCKNLPSSKMQNLDVMTDRKVSDDIPPGF-----PRPQNNTKLQKSQKFSTDAM 190
                                                                                                                                                                            NSECVRPQCSE - - -
                                                                                                                                                                                                                                                                                PVCKYEVLMENAQGPPLSHATVGDLVYHKWSCDGNNKEMYCMTVHSCVVDDGQGFGQKLV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDEERICAD---FRSVLVVSILLTVALIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVQNGICMSPFGFSMFMGLSIALIAAVII 375
                                                                                                                                                                                                             DEHGCTLDAFILKELEYNEKELEAGOMSSVFKFADKPTVFFSCMIRVEMKESAEMPCVIP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIDVRS--QNLEISQ-----LINITSSTMTPHPTEPPIQHTCPDIHVETESIEEASESKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYESCIMIENCELVGGE-ETHEVIDSSGCSKHESIMPQLEYHNRTHVGTSVKVFGVSHTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVSEITTAFQTQIVPM------PVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSET
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                                                                                                                                                                                                                                                                                                                                                                                                                             48/2; 137/3;
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                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                      ----EPENIID------VRTDI---NTLEISDDNQALP----VD 329
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                                                                                                                                                                                                                                                                                                                                                                                                                            180/3; 219/2; 255/1; 302/3
                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 290.5; DB 2; 27.4%; Pred. No. 1e-17; tive 45; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
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                                                                                                                                                                          ----PQGFGAVKTGGAAAKPAAAAQLRLLKKRSA--- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      November 1996
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                                                                                                                                                                                                                                                                                                                                                        Indels
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301
                                                                   250
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RESULT

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A; Molecule type: DNA
A; Residues: 1-514 <SCH>
A; Cross-references: EMBL:AF016429; PIDN:AAB65365.1; GSPDB:GN00023; CESP:T21H3.
A; Experimental source: strain Bristol N2; clone T21H3
C; Genetics:
                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cost A;Reference number: Z21077 A;Accession: T31736 A;Status: preliminary; translated from GB/EMB)
                                                                                       A;Gene: CESP:T21H3.4
A;Map position: 5
A;Introns: 54/1; 120/3;
                                                                                                                                                                                                                                                                                                                                                                                                  R;Scheet,
                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T21H3.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tcC;Accession: T31736
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: A88396
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: M01E10.2
A;Map position: 3
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A; Residues: 1-1286 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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  Local Similarity 19.0 nes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 VARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFY--MEADKTVSAQIEV--SEI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYASDDVERKFAFVDPRGCSSDLALLTDLTYADDSLTAWAASHVFNVHDAESLKFVCKLS 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIAETISLSTLPPTCTYSIRKEGPEGPIVSRAVVGQTVWHRWECDGTNDTNQAYGIQVHS 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPF-----DSCN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITIKEPNS-ECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIID-----
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                                                                                         165/2; 209/3; 355/2; 382/3; 456/1
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                     7.5%;
    63;
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Score 151.5; DB 2;
Pred. No. 3.1e-05;
3; Mismatches 108;
                                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
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                                           Length
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Indels 115;
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16;
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A; Decuse type: DNA
A; Molecule type: DNA
A; Residues: 1-3507 <FAV>
A; Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1
A; Cross-references: Strain Bristol N2; clone ZK783
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R;Favello, A.; Vaudin, M.

submitted to the EMBL Data Library, August 1994

submitted to the sequence of C. elegans cosmi
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c;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: ZK783.1
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Best Local
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3449
                                                                                                                                                                              3338 HCDVQLLDNHT-----MASTVVVQKHAMFLTNKADSYDLRCQYPIGSRAVESHVNVSELA 3392
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                                                                                                                                                                                                                                                                                                                                                            y Match 7.0%; Score 141; DB 2;
Local Similarity 21.5%; Pred. No. 0.0037;
hes 44; Conservative 44; Mismatches 99
                                                                                                                                                                                                                       81 SCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEI- 139
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                                                                                                                                                                                                                                                                                                               26 EGEPEIECGPTSITINFNTRNA-FEGHVYVKGLYDQEGCRND----EGGRQVAGISLPFD 80
                                        F-VDDGNGDTVEILNADGCALDKYL
                                                                                                                                                                                                                                                                    QGKLSVYCEADGMTLVLGNETADFEGKIFVKGQAENPYCSKSFSSLLNSRKPYVFKVVFQ 3337
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FAINIESGERYTLTDDMGCAIDESL 3473
                                                                                      TTSTLTEKNSTLAPICRLSV--SNDQHSSISSAMVGDTL-
                                                                                                                                 --TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPEEMTIEQRLLRIHELMKVKRENITVEVGRPT-----KKLLSHGAVPL
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                                                                                      -KLALEVTPSENFGILPRNC
                                                                                                                                                                                                                                                                                                                                                                                                            Length 3507;
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hypothetical protein T23F1.5 - Ca C; Species: Caenorhabditis elegans

Caenorhabditis elegans

RESULT 26 T25168

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submitted to the EMBL Data Library, October 1996
A; Reference number: Z19990
A; Accession: T25168
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1262 <WIL>
A; Cross references: EMBL: Z81129; PIDN: CAB03404.1; GSI
A; Experimental source: Clone T23F1
C; Genetics:
A; Gene: CESP:T23F1.5
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                                                                          A; Map position: X
A; Introns: 31/1;
                                                                                                      A; Gene: CESP:T24C2.1
                                                                                                                   A; Experimental source: C; Genetics:
                                                                                                                                A;Cross-references: EMBL:Z68120; PIDN:CAA92199.1; A;Experimental source: clone T24C2
                                                                                                                                                                                                     A;Reference number:
A;Accession: T25228
                                                                                                                                                                                                                  submitted to the EMBL Data A; Reference number: Z20000
                                                                                                                                                                                                                                            hypothetical protein T24C2.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T25228 R;Baynes, C.
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A; Residues: 1-665 <WIL>
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C;Accession: T25168
R;Wilkinson, J.
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A; Introns: 49/3;
    Best Local
Matches
                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                          FGFSMFMGLSIALIAAVIITISFK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSAEPENII-DVRTDINTLEISDDNQALPV--DLRHRALLQHNGQPVILAAVQNGICMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MVPES-DAYGMHIRNCKVVDAVGKIDHTLIDEQGCSADLQIIDHPHYDTYHDTASSHMWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSETVDTFCAVVHSCFVDDGNGDTVE-ILNADGCALDKYLLNNLEYPT-DLMAGQEAHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                VTSPPNSILSDASSFIKHRRASVPSEVSPATQSVRTSICLSKSCRPDFSEEVR--ICVNT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKVPDMSSLQIKCDILICSNIKSSVTNTTSCED------IPSPPFCADV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KTVSAQIEVSEITTAFQTQIVPMPVCRYEI-LDGG--PTGQPVQFAIIGQPVYHKWT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCGVKNVGEQVDSRA-----QYHMQVVLIIDQGNGTNTLQSFMAQCVHQKVNYNKQ 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCNVART-RSLNPRGIFVTTTVVISFHPLFVTKVD-----RAYRVQCFYMEAD----
                                                        31/1; 57/3; 95/3; 141/2; 175/2; 196/3; 226/1; 25
ily: Caenorhabditis elegans hypothetical protein
     Similarity
35; Conser
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       Conservative
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20.8%;
                6.5%;
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       18;
    Pred. No. 0.00
3; Mismatches
                              Score 132.5;
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                                                                                                                                                                                                                                 November
. 0.0021;
                                                                       196/3; 226/1; 259/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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                              DB 2;
                                                                                                                                             GSPDB:GN00028;
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                             Length 665;
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    Indels
                                                                       328/3; 388/2;
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                                                                                                                                               CESP: T24C2
  5;
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  Gaps
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A; Gene: C34G6.6
A; Map position:
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1011 <STO>
A; Cross references: GB:chr_I;
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84; Conservative
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protein C34G6.6 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequenco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                    346 AAVQNGICM-SPFGFSMFMGLSIALIAAVIITISFKFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              635 LYLGLPKDFGMRPISLDNIDDNETGKNKTKKGEETPLKDEIEEFRQKRQAAEFRDCGLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577 TVPIGPPVEVKAEAIQTICNYEGIKVQINNGEPFSGVIFVKNKFDT--CRVEVANSNAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 SIPVDNGVEGEPE---IECGPTSITINENTRNAFEGHVYVKGLYDQEGCR----NDEGGR 70
IE-EGSICLNSVTVFAIFGTLAVLILGQTVVIAHYAVR
                                                                                                                                                                                                                                                                      YADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLR-----
                                                                                                                                                                                                                                                                                                                                                                            VVHSCFVDD------GNGDTVEILNADGC----ALDKYLLNNLEYPTDLMAGQEAHVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                    EANLIQPRGKIELGNPVL-MQLLNGDGTEQPLVQAKLGDILELRWEIMAMDDE-LDFF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LNPRGIFVTTTVVISFH---PLFVTKVDRAYRVQCFYMEADKTVSAQIEVS---EITTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVAGISLPF-----DSCNVARTRS------
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                                                                                                                                                             -LIKKRSAEPENII-----DVRTDINTLEISDDNQALPVDLRHRA----LLQHNGQPVIL
                                                                                                                                                                                                                    FDSSASIRVTCEVEIC----KGDCEPVECALT----GGVKKSFGRKKREVSNNIEEFETNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQTQIVPM------PVCRYEILDGGPTGQPVQFAIIGQPVYHKW---TCDSETVDTFCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLN--GTYKSTVVIQTNNLGIPGLYTSMDQLYEVSCDY---SSMLGGRVQAGYNMTVTGP
                                                                                                                                                                                                                                                                                                                        -VKNCHAEPGVAGGKAGAGEKLRLIDG-GCPTPAVAQKLIPGAIEIKSSAVKTTKMQAFR
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Pred. No. 0.04
77; Mismatches
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                                                                                                           PVAMSRASTLDLLREDAHEVQM
                                                       382
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hypothetical protein F38E11.4 - Caenorhabditis elegans c;Species: Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T21967
                                                                                                                                                                                                                                                                                                                                                                                            K; DOSSON, K.
submitted to the EMBL Data Library
A; Reference number: 219141
A; A; Accession: T19553
A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C29E6.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct_1999 #sequence_revision 15-Oct_1999 #te C;Accession: T19553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, January 1996 A; Reference number: Z19495 A; Accession: T21967
                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z72504; P
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-942 <WIL>
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A; Introns: 23/1; 68/3; 116/1; 210/1; 284/1; 307/1; 359/3; 539/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone F38E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: 268342; PIDN: CAA92773.1; GSPDB: GN00022; CESP: F38E11.4
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                                                                                  Qy
                                                                                                                                                                                                                A; Map position: 4
A; Introns: 21/3; 67/3; 145/2; 175/1; 243/3; 308/1; 415/2; 540/1; 616/3; 659/3; 708/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 NQLAALK-PKVEGDVKSEKVLMEIVR------NGQAVTTVPLGAEVSLRWTVIDET-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556 ELHIPPPTEDDSKCGGIESEPHKWDYNVVVERNDMKTPSLVTTKDKTFQVSCDFSKIADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 TVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVD 188
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  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GISLPFDSCNVARTRSLNPRGIFVTTTVVISFH----PLFVTKVDRAYRVQC-FYMEADK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 PVDNGVEGEPEI-----ECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFCAVVHSCFVDDGNG-----DTVEILNADGCALDKYLLNNLEYPTDLMAGQ----EAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLTSSEESEGRVKARLSTECRMSGISVSLKFATPTSGTIYIKDHF--SSCRQSFSNTSFA 555
  RTRSLNPRGIFVTTTVVISFHPLF----VTKVDRAYRVQCFYMEADKTVSAQIEVSEITT 141
                                           QCLPQGINITFDLTQNTKYTGVVYASERFDQ--CRVFVKNSSAFSIFIPRPKHNSWCNAV 657
                                                                                       ECGPTSITINFN-TRNA-FEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDS----CNVA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
52; Conserv
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                                                                                                                                    Conservative
                                                                                                                                5.5%; Score 110.5; DB 2; 22.5%; Pred. No. 0.29; tive 38; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library,
                                                                                                                                                                                                                                                                                                                                PIDN:CAA96604.1; GSPDB:GN00022; CESP:C29E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 751;
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                                                                                                                                  Indels
                                                                                                                                                                           Length
                                                                                                                                                                              942;
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                                                                                                                                Gaps
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RESULT 31
T19902
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A; Molecule type: DNA
A; Residues: 1-446 <WIL>
A; Cross-references: EMBL: Z47067; PIDN: CAA87330.2; GSPDB: GN00028; CESP: C43C3.3
A: Pyparimental source: clone C43C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C43C3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A; Introns: 31/1; 64/3; 106/3; 153/2; 201/1; 233/2; 252/3; 286/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                       KPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQAL 326
                                                                                                                                                        ISPKECTFSDREDISAPDAKKITF--VQGGCPVNGMND--
                                                                                                                                                                                                                                       FSDVSNGHEVIASTGGKPKP--KVEMLFRSTDSGKTLQAARENEFVEFFIALSPDSAYHG 205
                                                                                                                                                                                                                                                                        VSEITTAFQ----TQIVPMPVCRYEIL----DGGPTGQP-----VQFAIIGQP--VYHK 179
                                                                                                                                                                                                                                                                                                                                                      PFDS-CNVARTRSLNPRGIFVTTTVVISFH-PLFVTKVDRAYRVQCFYMEADKTVSAQIE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVRSTSEEN -- SIRVDRRLLVKGDKNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKKRSAEPENIIDVRTDINTLEISDDNQA
  SNLTAERLRFRHKRS-----ITDLERRTTRSAPTDDNGSL 329
                                                                              NVNDQIYESKERTEREGNQSTVEVHCQVQVCLKK--DECSK-TCYKK--
                                                                                                   VDCIADSFTVVLNKSDPEVMRMISNPKSQPVVYVYGHKTRHPCGTSMKDEKGLINFNLTI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A--FRIDGSEQIDVVCIISIC--DENKKCPLMACTSPAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSNVSAELLRIVDCTAHRV---GGTGPPASVNLIADGCALLPAIMSPMRLTPSGWQSSLS 806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GIVVGGPSPVMITKKSHIHEKISLEITKDGQMVESVFVGESLLATV 749
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                                                                                                                                                                                              WT-----CDSETVD-----TFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLE 226
                                                                                                                                                                                                                                                                                                             PYGSECDVTLTDL--PKHRYAETTVVLEDNADLSFGKTTRLNHVFCLYTRNVKT----IR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
77; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%; Score 108; DB 2; L
22.6%; Pred. No. 0.17;
ative 47; Mismatches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 446;
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                                                                                                                                                      ·IIDPLA 247
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                                                                              -VSD
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RESULT 32 B89614

protein C43C3.3 [imported] C; Species: Caenorhabditis ele

elegans

Caenorhabditis

elegans

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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: B89614
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wust1.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: B89614
A;Status: preliminary
A;Residues: 1-495 <STO>
A;Cross-references: GB:chr_X; PIDN:CAA87330.1; PID:g3874884; GSPDB:GN00028; CESP:C43C3.3
A;Note: cDNA EST EMBL:T01034 comes from this gene
C;Gene: C43C3.3
A;Map position: X
                                                                                 A;Gene: galU;
C;Superfamily:
                                                                                                                       A; Experimental source: strain PAO1 C; Genetics:
                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-279 <STO>
A;Cross references: GB:AE004628; GB:AE004091; NID:g9948018;
                                                                                                                                                                                                                                            R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83394
                                                                                                                                                                                                                                                                                                                                                                                     UTP-glucose-1-phosphate uridylyltransferase PA2023 [imported] C:Species: Pseudomonas aeruginosa C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change C:Accession: A83394
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Best Local S
Matches 77
                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQAL 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSDVSNGHEVIASTGGKPKP--KVEMLFRSTDSGKTLQAARENEFVEFFIALSPDSAYHG
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                                                                           Escherichia coli UTP-glucose-1-phosphate uridylyltransferase
    Conservative
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5.0%; Score 102; DB 2;
21.9%; Pred. No. 0.3;
tive 32; Mismatches 89
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Pred. No. 0
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hypothetical protein F47G9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22367; T24409
R;White, S.
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A; Introns: 62/1; 181/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-828 <WIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: Z19887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:274035; PIDN:CAA98485.1; GSPDB:GN00023; CESP:F47G9. A;Experimental source: clone F47G9 R;Mortimore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T22367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z74041; PIDN:CAA98523.1; GSPDB:GN00023; CESP:F47G9.3
A;Experimental source: clone T03F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T24409
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A; Residues: 1-828 <WIL>
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                                    296 LLKKRSAEPENIIDVRTDINTLEISDDNQAL---PVDLRHRALLQHNGQPVILAAVQNGI 352
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                                                                                FRFKQGEAVKI - - ECEVKYCEK
LLDNATINIANCPSRNRRFTTFDESEDTTLTGNEDTEKVHAELLV---QTIVDSTQLDGY 788
                                                                                                                    HVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKT--GGAAAKPAAAAQLR
                                                                                                                                                             DNST-SARHVFVKKCTAYDQNGDEKIILIKNGCATQHAKEYVLRDEIKETATGFVLPFRA
                                                                                                                                                                                                     DSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALD - - - KYLLNN - - LEYPTDLMAGQEA
                                                                                                                                                                                                                                               AKTMNLRTTQFNKLDIYGKVNVKPMSMELRGKREII-----KARTVKLGQSLDLVFTV
                                                                                                                                                                                                                                                                                      QIEVSEITTAF -----QTQIVPMPV---CRYEILDGGPTGQPVQFAIIGQPVYHKWTC
                                                                                                                                                                                                                                                                                                                              LKIRHNDTTC-ITKNGDIYETVVVVTQNVESVGNATVITIDDQLFKVRCDYSNQKNAVAV 578
                                                                                                                                                                                                                                                                                                                                                                    AGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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peptidylglycine monooxygenase (EC 1.14.17.3) II precursor - African clawed frog N;Alternate names: C-terminal alpha-amidating enzyme II (AE-II); peptidyl alpha C;Species: Xenopus laevis (African clawed frog) C;aate: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Jun-1997 C;Accession: A27715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Xenopus laevis (Arrican claw
C:Date: 22-Nov-1993 #sequence_revision
C:Accession: 377855
R;Ohsuye, K.; Kitano, K.; Wada, Y.; Fuchimura, K.; Tanaka, Blochem. Blophys. Res. Commun. 150, 1275-1281, 1988
A;Title: Cloning of cDNA encoding a new peptide C-terminal A;Reference number: A27715; MUID:88134244; PMID:2829895
A;Accession: A27715
A;Molecule type: mRNA
A;Residues: 1-875 < OHS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine C;Keywords: oxidoreductase F;131-342/Domain: peptidylglycine monooxygenase I homology <PGM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Iwasaki, Y.; Kawahara, T.; Shimoi, H.; Suzuki, K.; Ghisalba, Eur. J. Biochem. 201, 551-559, 1991
A;Title: Purification and cDNA cloning of Xenopus laevis skin JA;Reference number: S17855; MUID:92037609; PMID:1935950
A;Accession: S17855
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-935 < IWA>
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N;Alternate names: peptidylhydroxyglycine N-C lyase
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov_1993 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVYKYADRSQL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQIEVSEI-TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTF
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                                                                               alpha-amidating
                                                                                                                      S.; Mizuno, K.; Matsuo,
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A;Experimental source: Skin
C;Comment: This copper protein is one of two enzymes that catalyze the oxidation of process of the corresponding desglycine peptide alpha-amide le and dismutates to glovaylate and the corresponding desglycine peptide alpha-amide hormones. The other enzyme is peptidyl alpha-amidating enzyme I.
C;Superfamily: peptidylglycine monooxygenase II; peptidylglycine monooxygenase I home C;Keywords: copper; glycoprotein; monooxygenase; oxidoreductase; transmembrane protein; 1-24,Domain: signal sequence #status predicted <SIG>
F;24-39/Domain: propeptide #status predicted <PRO>
F;24-39/Domain: propeptide #status predicted <PRO>
F;40-385/Product: peptidylglycine monooxygenase II #status predicted <MAT>
F;46-787/Domain: transmembrane #status predicted <TMNN>
F;465,662,743/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SM1
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1589 <JIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z22092; MUID: 98180948; A; Accession: T42233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Jiang, W.; WOitach, J.T.; Keil, R.L.; Bhavanandan, V.P. Biochem. J. 331, 193-199, 1998
A;Title: Bovine submaxillary mucin contains multiple doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submaxillary mucin 1 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                               1346
                                                                                                                                                                                                1293
1399 LKECPSPPTCKPEE---RLVKFKDNDTCCEIAYCEPRTCLFNNNDY
                                              189
                                                                                                                                               132
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                                                                                                                                                                                                                                                                                                                                           21 VDNGVEGEPEIECGPTSITINFNTR-NAFEGHVYVKGLYDQEGCRNDEGGR-----Q 71
                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQPTDVAVDPITGNFFVADGY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNP
                                                                                               GEQE-TETKTGCTTSLPPPPACY--
                                                                                                                                               AQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTC-DSETVD--
                                                                                                                                                                                                VTGVS-ESSSPGTSKEASETSTGPGISTTGSTSKS----NRITTSSRIP--YPETTVVAT 1345
                                                                                                                                                                                                                                            VAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQIEVSEI-TTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTF
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                                                                                                                                                                                                                                                                                               IQTGITGTGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QIKHQEFGREVFAVSYAP----
                                           -TFCAVVHSCFVDDGNGDTVEILNADGCALDKY-----LLNNLEYPTDLMAGQEAHVYK 241
                                                                                                                                                                                                                                                                                                                                                                                              62;
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                                                                                                                                                                                                                                                                                          -GTTSSPGGFNAEATTFKEHVRTTETRILSGTSTGVGRQTSTAVVSGR 1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.78;
21.68;
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22.3%;
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Pred. No. 6.7;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GG-----VLYAVNGKPYYG----DSTPVQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from
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                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                               -GPLGEKKSPGDIWTANCHKCTCTDAETVDCK 1398
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Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5 C; Epecies: Schizosaccharomyces pombe C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change C; Accession: T11616 F. Rajandream, M.A.; Walsh, S.V.; Wood, V. Submitted to the EMBL Data Library, October 1995 A; Reference number: 217300 A; Accession: T11616
                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2244 <BAR>
     A; Residues: 1-2244 < A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-649 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SPAC4H3.03c - C; Species: Schizosaccharomyces pomb
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A; Accession: T38883
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                                                                                                                                                                                                                                                                                                             NLEEVELTHLRG--YYNSHPVRIGNAAVHH
                                                                                                                                                                                                                                                                                                                                               AL-PVDLRH-RALLQHNGQPVIL--AAVQN 350
                                                                                                                                                                                                                                                                                                                                                                                     WIRDSAFTIYALAQLGFRAEAVEYMSFIYHVLKKKNKDGGINIV-----YSIHGDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                               --GGAAAKPAAAAQL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMEADKTVSAQIEVSEIT-TAFQTQIVPMPVCRYEILDGGPTGQ------PVQFAI 171
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EMBL: 254328; NID: g1009451; PID: g1009456
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                                                                                                                                                                                                                                                                                                                                                                                                                           -RLLKKRSAEPE-NIIDVRTDINTLEISDDNQ
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DNGVEGEPEIE----

-CGPTSITINFNTRNAFEGHVYVKGLYDQEGCRN- 65

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R; Matthews, L. submitted to the EMBL Data submitted to umber: Z19569
                                                                                                                                                      A;Cross-references: EMBL:Z82268; PIDN:CAB05199.1; GSPDB:GN00022; CESP:F52B11.3
A;Experimental source: clone F52B11
                                                                                                                                                                                                                                                                                                                       hypothetical protein F52B11.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T22486
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
T22486
                                                                                  A; Introns:
                                                                                                                     A; Gene: CESP:F52B11.3
                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-741 <WIL>
                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T22486
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A:Map position: IL
A:Note: SPAC22G7.06c
C:Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology;
arbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-p.
C:Keywords: ligase
                                                                                                A; Map position:
                                                                                                                                                                                                                                 A; Status: preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;61-440/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing)
F;265-440/Domain: trp6 homology <TR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;476-926/Domain: biotin carboxylase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;61-1519/Domain: carbamoyl-phosphate synthase (ammonia) homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain C; Genetics:
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3; Mismatches
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                                                                                                        587 VGPVEQDFDKNRLKSDLRAFRLDGSYDVQIVCSIM-----FCAGPNGCPVSNCLDS 637
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SIGNAL
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EMBL; Z49125; CAA88934.1; -.
PIR; A49772; A49772;
WORMPep; C4762.1; CE02165.
InterPro; IPR001507; Endoglin/CD105
SMART; SM00241; ZP; 1.
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=6239;
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                                                Signal;
 ; Repeat.
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1 YEW2_YEAST 1 PYR1_YEAST 1 YF61_METJA 1 CTPB_MYCLE 1 CADH_MOUSE 1 TYCB_BACBR 1 RNHL_HUMAN 1 RP54_BACSU 1 GLI_CHICK 2 GLI_CHICK 3 RRPP_MEASI 1 RRPP_MEASI 1 SM3E_CHICK
YEW2_YEAST PYR1_YEAST YF61_METJA CTPB_MYCLE CADH_MOUSE TYCB_BACBR TNYCB_BACBR TNHL_HUMAN RP54_BACSU GLI_CHICK ZPB_FELCA RRPF_MEASI SM3E_CHICK

## ALIGNMENTS

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CUT1_CAREL STANDARD
Q03755; Q18693;
Q1-FEB-1994 (Rel. 28, C
15-JUL-1998 (Rel. 36, L
15-DEC-1998 (Rel. 37, L
Cuticlin 1 precursor.
CUT-1 OR C47G2.1.
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: COMPONENT OF THE CUTICLES. IT FORMS A RIBBON
APPROXIMATELY 2 MICRONS WIDE RUNNING ALONG THE LATERAL LINES
UNDERNEATH THE ALAE. CONTRIBUTES TO THE FORMATION OF EXTRACELLULAR
ENVELOPES PROTECTING THE ORGANISM FROM THE ENVIRONMENT.

-- SUBCELLULAR LOCATION: Secreted.

-- TISSUE SPECIFICITY: LOCALIZED IN A NARROW BAND NOT EXPOSED
TO THE EXTERIOR, RUNNING UNDERNEATH THE ALAE.

-- IDEVELOPMENTAL STAGE: EXPRESSED DURING DAUER LARVA FORMATION.

-- DOMAIN: THE SMALL REPEATS A-A-P-[AVI] ARE ALAO PRESENT IN MANY
PROTEINS CONSTITUTING THE PROTECTIVE ENVELOPE OF OTHER SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
MEDLINE-91323673; PubMed-1864469;
Sebastiano M., Lassandro F., Bazzicalupo P.;
Sebastiano M., Lassandro F., Bazzicalupo P.;
"cut-1 a Caenorhabditis elegans gene coding for a dauer-specific noncollagenous component of the cuticle.";
Dev. Biol. 146:519-530(1991).
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Q09276;
Q1-NOV-1997 (
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16-OCT-2001 (
Hypothetical
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                   Durbin R.;
Submitted (OCT-2000)
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22 STRAIN-ATCC 15692 / PAO1;

23 STRAIN-ATCC 15692 / PAO1;

24 STOVER C.K., Pham X. O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

25 A Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

26 Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

27 A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

28 A Brody L.L., Coulter S.N., Folger K.R., Kas A., Paulsen I.T.,

29 A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

27 AR Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

28 "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

29 Opportunistic pathogen.";

20 L Nature 406:959-964(2000).

21 C -!- FUNCTION: MAY PLAY A ROLE IN STATIONARY PHASE SURVIVAL (BY
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Q9I291;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
pyrophosphorylase) (UDPGP) (Alpha-D-glucosyl-1-phosphate)
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ACC4B69B30032D84 CRC64;
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O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
O1-NOV-1997 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (Alpha-D-glucosyl-1-phosphate pyrophosphorylase).
                                                                                                                                                                             Chang H., Lee C., Peng H.;
"Identification and characterization of UDDglucose pyrophosphorylase encoding gene in Pseudomonas aeruginosa ATCC10145.";
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY PLAY A ROLE IN STATIONARY PHASE SURVIVAL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00483; NTP_transferase; 1.
TIGRFAMS; TIGR01099; galU; 1.
Transferase; Nucleotidyltransferase; Complete proteome.
SEQUENCE 279 AA; 31236 MW; 889B6B8639F159B2 CRC64;
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Q59633;
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                                           use
                                                             the
                                                                                                                                            SIMILARITY).
-i- CATALYTIC ACTIVITY: UTP + alpha-D-glucose 1-phosphate
                                                                                                                                                                                                                                                        STRAIN-ATCC 10145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004628; AAG05411.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                               modified and
                                                                                                                   diphosphate + UDP-glucose.
-!- SIMILARITY: BELONGS TO THE PROKARYOTIC UDPGP FAMILY.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
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by non-
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                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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            non-profit institutions as long as its con
and this statement is not removed. Usage by
requires a license agreement (See http://www
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   email to
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01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptidyl-glycine alpha-amidating monooxygenase II pr
(EC 1.14.17.3) (Peptide C-terminal alpha-amidating e
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Battrachia; Anura; Mesobatrachia; Pipoidea;
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                                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae;
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                                                                                                                                                                                                                                                                                                       "Cloning of cDNA encoding a new peptide C-terminal alpha-amidating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                     CATALYTIC ACTIVITY: Peptidylglycine + ascorbate + O(2) peptidyl(2-hydroxyglycine) + dehydroascorbate + H(2)O. COFACTOR: COPPER AND ASCORBATE.
                                                                                                                                                                                                                       FUNCTION: C-terminal alpha-amidation of peptides. The reaction produces a peptidyl(2-hydroxyglycine) intermediate is unstable dismutates to glyoxylate and the corresponding desglycine peptitudes.
                                                                                        European Bioinformatics Institute.
                                                                                                   SWISS-PROT entry is copyright. It is produced through the the Swiss Institute of Bioinformatics and the EM
                                                                                                                                             MONOOXYGENASE FAMILY.
                                                                                                                                                          SIMILARITY: BELONGS TO THE COPPER TYPE
                                                                                                                                                                                                              amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVAGISLPFDSCNVARTRSLNPRGI---FVTTTVVISFHPLFVTKVDRAYRVQCFYMEAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPVDN-----GVEGEPEIECGPTSITI-NFNTRNAFEGHVYVKGLYDQEG-CRNDEGGR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVLTQMVKLYQKYRCTIVAVMEVNPTETNKYGVIAGDDIGDGLIRVRDMVEKPAPEDAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTVSAQIEVSE---ITTAFQTQIVPMPVCRYEILDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLVGIRKLLDECSFSYTRQTQMKGLGHAILTGRPLIGDEPFAVVLADDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPVVNKPLIQYGV--EEALDAGLNEISIVTGRGKRALEDHFDIS--YELENQIKGTDKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00483; NTP_transferase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                   Wada
                                                                                                                                                                                                                                                                  Commun. 150:1275-1281(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TPDIFKLIEET---EPGKGGEIQITDALLKQAKDGCVI 244
                                                                                                                                                                                                                                                                                           membrane-spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                 Fuchimura K.,
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0.35;
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                                                             Usage
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                                                                         are no restrictions its content is in
                                                                                                                                                          ASCORBATE - DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              II precursor
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                                                               and
                                                                                                                                                                                                                                                                                           Xenopus
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                                                                                                      EMBL outstation
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                                                                                                      a collaboration
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EMBL; M19032; AAA49667.1;

or send an email to license@isb-sib.ch)

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RESULT YAYS LANGE AND LANG
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Best Local
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., Mononey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
                                                                                                                                                                                                                                                                                                                                                                           Q10211;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C4H3.03c in chromosome I.
SPAC4H3.03C.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                         MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M
                                                                                                                                                                                                                                                                    Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                 Schizosaccharomycetales;
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Pfam;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00790; PAMONOXGNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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erPro; IPR000720; Pamonoxygen;
n; PF01082; Cu2_monooxygen; 1.
n; PF0135; NHL; 4.
n; PF03712; Cu2_monoox_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAVVHSCFVDDGNGDTVEILNADGCALDKYL--LNNLEYPTDLMAGQEAHVY
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21.6%;
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POLY-GLU

POLY-ASP.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------CN-SRIMQFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649
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Matches 86
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Skelton J., Simmonds M., Squares R., Squares K.,

RA Haylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA BORZym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,

Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Moreno S., Armstrong J., Forsburg S.L.,

RA Daga R.R., Cruzado L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

The genome sequence of Schizosaccharomyces pombe.";

Nature 415:871-880(2002)

"Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
TRANSMEM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Rutherford K., Rutter
   355
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                                                                           303
                                                                                                             282
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                                 AL-PVDLRH-RALLQHNGQPVIL--AAVQN 350
                                                                       WIRDSAFTIYALAQLGFRAEAVEYMSFIYHVLKKKNKDGGINIV----
NLEEVELTHLRG--YYNSHPVRIGNAAVHH
                                                                                                           --GGAAAKPAAAAQL---
                                                                                                                                           YWRAWIQQCVYTGRYREFVQRNALTLKLLIYEPTGAVIASPTFSLPEDLGGVRNWDYRFT
                                                                                                                                                                  MAGQEAHYYKYADRSQLFYQ---CQISITIKEPNSECV-RPQCSEPQGFGAVKT-----
                                                                                                                                                                                                                                                                                                                                                                YEPSTNILHTKFYSERGYL---RLLDFFHRPWEDYEPLYPWLIRRVSCIRGTSRIKLECF
                                                                                                                                                                                                                                                                                                                                                                                                                                        LDGSVEMMCWP----NFDSPSIFARILDARAGHFSITPI-EQTSCK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGEPEIECGPTSITINENTRNAF-----EGHVYVKGLYDQEGCRNDEGGRQVAGISL 77
                                                                                                                                                                                                                   EGGGVISYLELEEGQEITF - - - - - IFRQEGLGPNVDYVTPN - - - - -
                                                                                                                                                                                                                                                     IGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDL
                                                                                                                                                                                                                                                                                         PALDYARQSHETRVSKITENYYQAEFVPASGDPKYILDCVPSGDQLKIDLELIYPAEHLI
                                                                                                                                                                                                                                                                                                                            YMEADKTVSAQIEVSEIT-TAFQTQIVPMPVCRYEILDGGPTGQ------
                                                                                                                                                                                                                                                                                                                                                                                                  PFDSCNVARTRSLNPRGIFVTTTVVISFH------PLFVTKVDRA-----YRVQCF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 4.6%;
Similarity 22.1%;
36; Conservative 5:
                    <u>:</u>
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626
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265 28
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584
646
74488
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5 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93.5; DI
Pred. No. 1.8;
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                       -- RLLKKRSAEPE-NIIDVRTDINTLEISDDNQ
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RESULT 7
PYR1\_SCHPO

PAC ID

PYR1\_SCHPO STANDARD; 009794; 01-NOV-1995 (Rel. 32, Created)

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modified and this statement is not removed.

Usage

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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Leather S., McDean J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Nell S., Pearson D., Ouall M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gaffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Bandan R.R., Cruzado L., Jinenez J., Sanchez M., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
"The genome seguence of Schizosacchar M. Dreas P.,

"Th
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Curr. Ge
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002)
-i- FUNCTION: THIS PROTEIN IS A "FUSION" PROTEIN ENCODING
ENZYMATIC ACTIVITIES OF THE PYRIMIDINE PATHWAY (GATASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
URA1 protein [Includes: Glutamine-dependent carbamoyl-phosphate
synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3.2)].
URA1 OR SPAC22G7.06C.
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembled on a multifunctional protein including a dihydroorotase-like cryptic domain in Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21848401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                               + N-Carbamoyl-L-aspartate.

PATHWAY: Pyrimidine biosynthesis; first step.
PATHWAY: Pyrimidine biosynthesis; second step.
PATHWAY: Pyrimidine biosynthesis; second step.
MISCELLANEOUS: GATASE (GLUTAMINE AMIDOTRANSFERASE) AND CPS
(CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE
GLUTAMINE-DEPENDENT CPSASE (GD-CPSASE) (EC 6.3.5.5).
MISCELLANEOUS: IN EUKARYOTES EC 6.3.5.5 SYNTHESIZED BY
PATHWAY-SPECIFIC (ARGININE AND PYRIMIDINE) UNDER SEPARATE
SIMILARITY: THE CPSASE DOMAIN IS SIMILAR TO OTHER CPASES.
SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE DHOASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND ATCASE) (BY SIMILARITY).

CATALYTIC ACTIVITY: 2 ATP + L-glutamine phosphate + glutamate + carbamoyl phosphate CATALYTIC ACTIVITY: Carbamoyl phosphate
                                                                                                                                                                                                                            DEFECTIVE DO
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                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                   CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN
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sphate + L-aspartate =
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Pfam;
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InterPro;
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                                   1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00099; CPSGATASE.
PRINTS; PR00096; GATASE.
TIGREAMS; TIGR00670; asp.carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE;
PROSITE; PS00442; GATASE_TYPE_I; 1.
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InterPro; IPR002474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002082; Asp_carbmltransf.
InterPro; IPR001317; CPS_GATase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z54328;
HSSP; P00968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X81841; CAA57433.1; -. EMBL; Z54328; CAA91130.1; -.
             196
                                                                                                   96
                                                                                                                                            42 FWTRNAFEGHVYVKGLYDQEGCRNDEG-----GRQVAGISLPFDSCNVARTRSLNPRGI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         m; PF00289; CPSase_L_chain; 2.
m; PF00744; Dihydroorotase; 1.
m; PF007988; CPSase_sm_chain; 1.
m; PF02142; MGS; 1.
m; PF02729; OTCace_N; 1.
m; PF02786; CPSase_L_D2; 2.
m; PF02787; CPSase_L_D3; 1.
NTS; PR00100; AOTCASE.
NTS; PR00098; CPSASE.
 SCFVDDGNGDTV--EILNADGCALDKYLLNNLEYPTDL---
                                 ALPLHRENVKILGTSPEMIDGAENRFKFSRMLDDIGVDQPKWKELTSFDE-ADKFC----
                                                                                                 FVTTTVVISFHPLFVT----KVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQI----V
                                                                                                                         YTTYNAVEHDIHF -----
                                                                            ---KTIMVNYNPETVSTDYDEADRLY-FENIGLETVLDIYEQESSSGIIIAMGGQTANNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00117; GATase; PF00185; OTCace;
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00866; CPSASE_1; PS00867; CPSASE_2;
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IPR000991; GATase_1.
IPR004362; MGS_1ike.
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                                                                                                                                                                                                               248306
                                                                                                                                                                  58;
                                                                                                                                                                                                                       (BY SIMILARITY).

GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).

GATASE (BY SIMILARITY).

GIC -> RYF (IN REF. 1).

CAVRA -> LOFAQ (IN REF. 1).

EL -> DV (IN REF. 1).

G -> E (IN REF. 1).

G -> E (IN REF. 1).
                                                                                                                                                                                                               MW;
                                                                                                                         · NDKGVMVLGSGVYRIGSSVEFDWCAVRAVRTLRDRGV
                                                                                                                                                                              Score 92;
Pred. No.
                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
LINKER (BY SIMILARITY).
CPSASE (CARBAMOYL-PHOSPHATE
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                           LINKER (BY SIMILARITY).
ATCASE (ASPARTATE TRANSCARBAMYLASE)
                                                                                                                                                                                                                                                                                                                                                 DEFECTIVE DHOASE DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                           se; Transferase; Multifunctional enzyme GATASE (GLUTAMINE AMIDOTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                        LINKER (BY SIMILARITY)
                                                                                                                                                                                                             -> E (IN REF. 1).
-> E (IN REF. 1).
; 5700D153B50CD3E9
                                                                                                                                                                   Mismatches
                                                      GQPVQFAIIGQPVYHKWTCDSETVDTFCAVVH
                                                                                                                                                                                         DB
                                                                                                                                                                                         ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.isb-sib.ch/announce/
                                                                                                                                                                   153;
                                                                                                                                                                                        Length 2244;
-MAGQEAH---VYKYA
                                                                                                                                                                   Indels
                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                          <u>'</u>
                                                                                                                                                                   80;
                                                                                                                                                                  Gaps
                                                                                                   148
                                                                                                                         1048
                                  1159
                                                       195
                                                                             1104
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RESULT 8
NRK1_YEAST
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InterPro; IPRO00719; Euk_pkinase.

R InterPro; IPR002790; Ser_thr_pkinase.

R Pfam; pF00069; pkinase; 1.

R ProDom; pD000001; Euk_pkinase; 1.

R ProDom; pD000001; Euk_pkinase; 1.

R SMART; SM00220; S. TKC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

W Transferase; Serine/threonine-protein kinase; ATP-binding.

DOMAIN 23 276

T DOMAIN 29 37 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               Science 265:2077-2082(1994).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRK1_YEAST STANDARD; PRT; 1080 AA.
p38692;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase NRK1 (EC 2.7.1.37) (N-rich kinase NRK1 OR KIC1 OR YHR102W.
                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288c / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                         EMBL; D29980; BAA06250.1; -.
                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukami Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-DC-5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
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                                                                                                                                                                                                       $48944; $48944.
$0001144; KIC1.
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                                                                                                                                                                                                                                          U00059; AAB68860.1;
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cetaceae; Saccharomyces.
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RESULT 9
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Best Local S
Matches 45
                                                                                                                                                                                                                                           TUD_DROME
P25823;
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
ACT_SITE
SEQUENCE
                                 FlyBase; FBgn0003891; tud.
InterPro; IPR001997; Maternal_tudor.
InterPro; IPR002999; Tudor.
Pfam; PF00567; TUDOR; 10.
SMART; SM00333; TUDOR; 9.
                                                                                         EMBL; X62420; CAA44286.1;
PIR; A41519; A41519.
HSSP; Q16637; IG5V.
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
Dowelopmental DOMAIN 45
                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                        PROSITE; PS50304; TUDOR; 9
                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                      entities requires a
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92038995; PubMed=1936993;
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45; Conservative
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1080 AA;
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144
                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
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BY S
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SIMILARITY.
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RESULT 10
THRC_BUCAL
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AC P5728
DT 16-OC
DT 15-U
DE Three
GN THRC
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OS Buchr
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DOMAIN
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                                                                                                                                                                                Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS."; Nature 407:81-86(2000).

-!- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O = L-threon
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                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUCAI
                                                                                                                                                                                                                                                                                                         MEDLINE=20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=118099;
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16-OCT-2001
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                    STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                  phosphate.

COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

PATHWAY: Threonine biosynthesis.

SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
  European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLQLP-DAYISWSPEAEAKFAELTGEGELVFTTQLLKPGQDHVTIDLLLD------G 1953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EILDGGPT-----GQPVQFAIIGQPVYHKWTCDSE-----TVDTFCAVVHSC
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Pred. No.
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CGE1_CHICK
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CCNE1 OR CCNE.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004450; Thr_synthase.

Pfam; PF00291; PALP; 1.

Pfam; PF00291; PALP; 1.

TIGREAMS; TIGR00260; thrc; 1.

PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

Threonine biosynthesis; Lyase; Pyridoxal phosphate; Complete proteome.

BINDING 108 108 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                           P49707, 091032,
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
16-0CT-2001 (Rel. 40, Last ann
                                              G1/S-specific cyclin E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001926; B6_enzyme_beta
InterPro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP001118; BAB12909.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFSFKHPLK--IKITKDIHCFELFHGPTLAFKDFGARFMAQMILLLNKKNESVTILTATS 136
                                                                                                                                                                                                 EKILKNKISLPSELQNRIDLPLLSHNINPV
                                                                                                                                                                                                                             E-ISDDNQALPVDLRHR---ALLQHNGQPV 343
                                                                                                                                                                                                                                                                                       SECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTD-----INTL
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                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                       -GYVSEPHAAIAYRLLRDQLKENEFGLFLGTAHPAKFKNTV
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145;
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SEQUENCE FROM N.A.
Li H., Lahti J.M., Valentine M., Houston J., Kidd V.J.;
Li H., Lahti J.M., Valentine M., Houston J., Kidd V.J.;
The cyclin E gene is apparently essential in avian B ce.
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLI
(START) TRANSITION.
-i- SUBUNIT: INTERACTS WITH A MEMBER OF THE CDK2/CDK PRO:
TO FORM A SERINE/THREONINE KINASE HOLDENZYME COMPLEX
SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX
                                                                                                                                                                             Gallus
                                                                                                                                                                                          Archosauria;
                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                          Aves;
                                                                                                                                                                                          Neognathae;
                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                   THE CDK2/CDK PROTEIN KINASES OLOENZYME COMPLEX. THE CYCLIN
                                                                THE CELL CYCLE
                                                                                               cells.";
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      (BY
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Chordata;

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RESULT
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                                                                            SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004367; Cyclin_C
Pfam; PF00134; cyclin; 1.
Pfam; PF02984; cyclin_C; 1.
SMART; SM00385; CYCLIN; 1.
PROSITE; PS00292; CYCLINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                    110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).

SUBCELLULAR LOCATION: Nuclear (By Similarity).

SUBCELLULAR LOCATION: Nuclear (By Similarity).

PTM: PHOSPHORYLATION BY CDK2 TRIGGERS ITS RELEASE FROM CDK2 AND DEGRADATION VIA THE UBIQUITIN PROTEASOME PATHWAY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN E SUBFAMILY.
                                                                                                                              NIQTHINSLDLLDKAQA
                                                                                                                                                        DVRTDINTLEISDDNQA 325
                                                                                                                                                                                                        FYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENII
                                                                                                                                                                                                                                   QYPQQIFV-----QIAELL-.-DLCVLD---IGCLEYTYGVLAASALYHFSSSELMQKVSG
                                                                                                                                                                                                                                                                                                              CRYE-ILDGGPTGQPV--QFAIIGQPVYHKWTCDSETVDTFCAVV-----
                                                                                                                                                                                   YEWCEI - - -
                                                                                                                                                                                                                                                          ---HSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRSQL---
                                                                                                                                                                                                                                                                                     HQFAYVTDGACTEDEILSMELIIMKAL--NWNLNPLTVVSWLNIYMQVAYLNELYEVLLP
                                                                                                                                                                                                                                                                                                                                                                ---VTKVDRAYRVQCFYMEAD-------KTVSAQIEVSEITTAFQ-TQIVPMPV
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an email to license@isb-sib.ch).
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Cell cycle;
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407 F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell division; Phosphorylation; Nuclear protein.
392 PHOSPHORYLATION (BY SIMILARITY).
106 G -> G (IN REF. 1; AAA81647).
343 L -> S (IN REF. 1; AAA81647).
46739 MW; A1032C7CBOBCIDIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%;
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 407;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Jones M., Leather S., McLean J.,
RA Goliver K., O'Neil S., Parson D., Ouail M.A., Rabbinowitsh E.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Cliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsh E.,
RA Goliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsh E.,
RA Weltjens I., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gel Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G. V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
RT "The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a compete the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 1260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002821; Hydantoinase_A. InterPro; IPR003692; Hydantoinase_B. Pfam; PF01968; Hydantoinase_A; 1. Pfam; PF02538; Hydantoinase_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 268166; CAA92315.1;
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181
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Wood V., Gwilliam R., Rajandream א
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                                                                                                                                                                                                                                                     GPTSITINENTRNAFEGHVYVK-----GLYDQEGCRN---DEGGRQVAGISLPFDSCN
                                     EKAVRDVLKAFSVQNSQKPLKAIDYMDDGTPLQLEVKIDPETGDAVFDFEGTGPEVYGNW
                                                                               QIEVSEITTAFQTQIVPMPVCRYEILDGG
                                                                                                                        GSRTLRDNISDVKAMLSACHRGRSMVEKLVVEYGLDIVQR--SMYGIQ
                                                                                                                                                                                                            GITPGSMPSNSKAIYEEGAAIKTFKVVKAGTFDEKGLTQLLFDEPAK-----YPDCS
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                                                                                                                                                                                                                                                                                                                   4.3%;
                                                                                                                                                                                                                                                                                                                                                                                138784 MW; 44F14F0638224BBB CRC64;
                                                                                                                                                                  -PRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSA 132
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Pred.
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No. 19;
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                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                               111;
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ISCS_METTE
P57795;
                                                                                                                                                                                                                                                                                                             Lyase; Py
ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cysteine biosynthesis in the archaea: Methanosarcina thermophila utilizes O-acetylserine sulfhydrylsse.";
FEMS Microbiol. Lett. 189:205-210(2000).
-!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR FROM CYSTEINE TO PRODUCE ALANINE (BY SIMILARITY).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1154
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Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20389605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probable cysteine
                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000192; Aminotransfy.
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16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
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                           NGDTVEILNAD--GCALDKYLLNNLEYPTDLMA---
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                                                                IYFTSGGTESDNWAIKGIAFANRDKGKHIITSSIEHH------AVLHTCAWLEG
                                                                                                                                                                                                                                                                                                                                                                                                PF00266;
                                                                                                                                                                                                                                                                                                                                     Pyridoxal phosphate. TE 338 338
                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                 404 AA;
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41, Last annotation update)
desulfurase (EC 4.4.1.-) (NIfS protein
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                                                                                                          -QPVQFA----
                                                                                                                                                                                                                                                                                                                 44335 MW;
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                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                   Score 86; DB 1;
Pred. No. 4.5;
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87B5BA25F87E2A25 CRC64;
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DSG2_HUMAN
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01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cadherins.
Exp. Cell
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                   PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_2; 4.
Cell adhesion; Glycoprotein; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                 PRINTS; PR00205; CADHERIN. SMART; SM00112; CA; 4.
                                                                                                                       Pfam; PF00028; cadherin;
                                                                                                                                                                                     Genew; HGNC:3049;
                                                                                                                                                                                                         EMBL; Z26317; CAA81226.1; HSSP; P15116; INCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 777-1117 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Colon carcinoma;
MEDLINE-94192736; PubMed-8143788;
Schaefer S., Koch P.J., Franke W.W.;
"Identification of the ubiquitous hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                           InterPro; IPR002126; Cadherin
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SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
                                                                                                                                                                  125671;
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; Glycoprotein; Transmembrane;
Calcium-binding.
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glein subfamily of
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ac o4261;
AC 04261;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 41, Last annotation update)
DT 15-JUL-1998 (Rel. 41, Last annotation update)
DE HIRA protein (TUP1 like enhancer of split protein 1).
GN HIRA OR TUPLE1.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes:

NCBI_TaxID-31033;
N [1]
    HIRA_FUGRU
ID HIRA_F
AC 042611
DT 15-JUL
DT 15-JUL
DT 15-JUN
DE HIRA P
GN HIRA P
GN FUGU Y
OC EUKARY
OC ACATINO
OC ACATINO
OC TETTAO
OX NCBI_T
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RX MEDLIN
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Best Local
                                  Llevadot R., Estivill X., Scambler P., Pritchard M.;
"Isolation and genomic characterization of the TUPLE1/HIRA gene of
the pufferfish Fugu rubripes.";
Gene 208:279-283(1998).
-I- FUNCTION: Could have a part in mechanisms of transcriptional
regulation similar to that played by yeast HIR1 and HIR2 together.
-I- SUBCELLULAR LOCATION: Nuclear (Potential).
-I- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
-I- SIMILARITY: BELONGS TO THE HIR1 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-98201624; PubMed-9524281;
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ASSESSED REPEAT 3.
ASSESSED REPEAT 4.
DESMOGLEIN REPEAT 5.
DESMOGLEIN REPEAT 6.
N-LINKED (GLCNAC. . .) (POTENTININED (GLCNAC. . .) (
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RESULT 16
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01-NOV-1997 (Rel. 3
30-MAY-2000 (Rel.
                                                           Wilkerson C.G., King S.M., Witman G.B.;
"Molecular analysis of the gamma heavy chain
flagellar outer-arm dynein.";
J. Cell Sci. 107:497-506(1994).
-i- FUNCTION: FORCE GENERATING PROTEIN OF EUK
FLAGELLA. PRODUCES FORCE TOWARDS THE MINU
                                                                                                                                                                                          STRAIN-1132D;
MEDLINE-94274766;
                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorop
Chlamydomonadaceae; Chlamydomonas
                        <del>;</del>
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                                                                                                                                                                                                                                                                           NCBI_TaxID=3055;
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ProDom; PD000018; WD40; 3.
SMART; SM00320; WD40; 5.
PROSITE; PS00678; WD_REPEATS_1;
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                                                                                                                                              ENIIDVRTDINTL--EISDDNQALPVDLRHRALLQHNGQPVILA
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Bioinformatics Institute. There are no restrictions
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PIR; A39040; A39040.
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HSSP; P07221; 1A8Y.
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Muscle; (
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J. Biol. Chem. 266:391-398(1991).

--- FUNCTION: CALSEQUESTRIN IS A HIGH-CAPACITY, MODERATE AFFINITY, CALCIUM-BINDING PROTEIN AND THUS ACTS AS AN INTERNAL CALCIUM STOI IN MUSCLE. THE RELEASE OF CALCIUM BOUND TO CALSEQUESTRIN THROUGH A CALCIUM RELEASE CHANNEL TRIGGERS MUSCLE CONTRACTION. BINDS 40
                                                                                                                                                            CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slupsky J.R., Ohnishi M., Carpenter M.R., R. "Characterization of cardiac calsequestrin. Biochemistry 26:6539-6544(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91093153; PubMed=1985907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88107564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Hear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE OF 20-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete amino acid
by cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones L.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott B.T., Simmerman H.K.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88243763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASQ2.
                                                                                                                                                                                                                                          PRINTS; PR00312
                                                                                                                                                                                                                                                                   InterPro; IPR001393; Calsequestrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO 50 MOLES OF CALCIUM.

SUBCELLULAR LOCATION: THIS ISOFORM OF CALSEQUESTRIN OCCURS SURCELLULANIC RETICULUM'S TERMINAL CISTERNAE LUMINAL SPACES CARDIAC AND SLOW SKELETAL MUSCLE CELLS.

SIMILARITY: BELONGS TO THE CALSEQUESTRIN FAMILY.
                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                PS00863;
PS00864;
                                          410
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219
221
372
372
335
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                                                                                                                                                                                                            CALSEQUESTRIN.
; CALSEQUESTRIN_1; 1.
; CALSEQUESTRIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=3379055;
rman H.K.B., Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=3427023;
                                                       19
410
254
410
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71
                                          47416 MW;
    4.28;
20.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
                                                                                                                                                                                                   Calcium-binding; Signal; Phosphorylation.
    Score
Pred.
                                                     PHOSPHORYLATION (BY Q -> E (IN REF. 2).
                                                                                                       CALCIUM REGULATED HYDROPHOBIC SITE.
ASP/GLU-RICH (ACIDIC).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                               PHOSPHORYLATION PHOSPHORYLATION
                                                                                                                                                              PRO-RICH.
                                                                                                                                                                         CALSEQUESTRIN, CARDIAC MUSCLE ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0f
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                                          FCA99A8D7E7ABB82 CRC64;
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  NO.
6.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiac
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n.";
                DB
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                                                                  CK2).
               Length 410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.A.F
                                                                                                                                                                                                                                                                                                                                                                                                                        igh a collaboration EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLG_EC12T STANDARD; PRT; 2193 AA.

POLG_EC12T STANDARD; PRT; 2193 AA.

066575; 066576;
15-UL-1999 (Rel. 38, Created)
15-UL-1999 (Rel. 38, Last sequence update)
15-UL-1999 (Rel. 38, Last sequence update)
15-UL-1999 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 38, Last sequence update)
15-UN-2002 (Rel. 38, Las
    use by modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Wild type;
MEDLINE=95364006; PubMed=7637032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kraus W., Zimmermann H., Zimmermann A., Eggers H.J., Nelsen-Salz
"Infectious cDNA clones of echovirus 12 and a variant resistant
against the uncoating inhibitor rhodanine differ in seven amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Enterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=103909;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol.
                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                             SIMILARITY: P2A PROTEASE BELONGS TO PEPTIDASE FAMILY C3. SIMILARITY: P3C PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Selective creavage or war policytrus reactions Glu ma substituted for Gln, and Ser or Thr for Gly.

CATALYTIC ACTIVITY: Selective creavage of Tyr-|-Gly bond in the catalytic catalytic catalytic catalytics.
                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITO1. 69:5853-5858(1995).
FUNCTION: P2A AND THE P3C POLYPEPTIDES ARE PROTEASES THAT CLEAVE AT CERTAIN Q/G SITES IN THE POLYPROTEIN. THEY ARE CYSTEINE
                                                                                                                                                                      CLEAVAGE BETWEEN VP4 AND VP2 IS AUTOCATALYTIC; VP1/P2A IS CATALYZED BY P2A; ALL OTHER CLEAVAGES ARE CATALYZED BY P3C.
                                                                                                                                                                                                                                                                              SUBUNIT: THE VIRUS CAPSID
                                                                                                                                                                                                                                                                                                                                       picornavirus polyprotein. In other picornavirus be substituted for Gln, and Ser or Thr for Gly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEMDEPIAI - - - - - - PDKPYTEEELVEEVKEHQRPTLRRLRPEDMEETWEDDLNGIHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNLEYPTDLMA----GQEAHVYKYADRSQLFYQCQI------SITIKEPNSECVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAKKLGFDEEGSLYVLKGDRTIEFDGEFAADVLVEFLLDLIEDPVEIINS---KLEVQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTKVDRAYRVQCFY----MEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDG----GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVYVKGLYDQEGCRNDEGGRQVAGISLP-FDSCNVARTRSLNPRGIFVTTTVVISFHPLF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQCSEPQGFGAVKTGGAAAKPAAAAQL-RLLKK-----RSAEPENIIDV-RTDINTLEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                            NIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS AND VP4.

SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE
    non-profit
and this si
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                                                                                                                                                                                                                                                          OF 60 ICOSAHEDRAL EACH OF PROTEINS V
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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RNA-directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities regulres a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001306; Pico_P2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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MEROPS; C03.022;
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SITIKEPNSECVRPQCSEPQGFGAVKTGG
                                         TTAHGCDTIARCQCTTGVYFCASRNKHYPVSFEGPGLVEVQESEYYPRRYQSHVL----L
                                                                                   LNADG
                                                                                                                                                                                                                                                   TVVISFHPLFVTK-VDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEIL 158
                                                                                                                                                                                                                                                                                               GNAPARMSIPFISIGNAYSNFYDGWSHFTQDGVYGFNSLNNMGSIYIRHVNEQSPYAITS
                                                                                                                                                                                                                                                                                                                                         GRQVAGISLPFDSCNVART-----VTT
                                                                                                                             NTGAFGQQSGAAYVGNYRVVNRHLATHVDW
                                                                                                                                                                    DGGPTGQPVQFAIIGQ------PVYHKWTCDSETVDTFCAVVHSCFVDDGNGD-TVEI
                                                                                                                                                                                                              TVRVYFKPKHVRAWVPRPPRL-CAY---EKSSNVNFKPTDVTTS-RTSITEVPSLRPSVV
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X77708; CAA54783.1; -.
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IPR000199; Cys-protease-3C.
IPR003138; Pico_PlA.
IPR000081; Pico_P2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002527; Pico_P2B.
IPR000605; RNA_helicase.
IPR001205; RNA_pol_P3D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cys-protease-3C;
RNA_dep_RNA_pol;
RNA_helicase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pico_P1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pico_P2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pico_P2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymerase;
                                                                                 -CALDKYLL--NNLEYPTD-----LMAGQEAHVYKYADRSQLFYQCQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2094
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1709
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228
376
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725
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568
859
1009
1108
1437
1526
1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2193 RNA-DIRECTED RNA POLYMERASE.
2 MYRISTATE (BY SIMILARITY).
1695 PROTEASE 3C (POTENTIAL).
1709 PROTEASE 3C (POTENTIAL).
1709 PROTEASE 3C (POTENTIAL).
223 H -> Y (IN RHODAMINE-RESISTANT VA
228 G -> S (IN RHODAMINE-RESISTANT VA
228 G -> C (IN RHODAMINE-RESISTANT VA
376 I -> M (IN RHODAMINE-RESISTANT VA
643 Y -> C (IN RHODAMINE-RESISTANT VA
643 Y -> A (IN RHODAMINE-RESISTANT VA
725 V -> A (IN RHODAMINE-RESISTANT VA
725 V -> A (IN RHODAMINE-RESISTANT VA
726 V -> R (IN RHODAMINE-RESISTANT VA
2094 C -> R (IN RHODAMINE-RESISTANT VA
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                                                                                                                                                                                                                                                                                                                                                                                                       4.1%;
22.3%;
                                                                                                                                                                                                                                                                                                                                                                                 31;
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CORE PROTEIN P2B.
CORE PROTEIN P2C.
CORE PROTEIN P3A.
                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME-LINKED PROTEIN PICORNAIN 3C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Thiol protease COAT PROTEIN VP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COAT PROTEIN VP1
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN VP3
                                                                                                                                                                                                                                                                                                                                                                                                         NO .
                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                             ONCVWEDYNRDLLVST
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2193;

VARIANT).
VARIANT).
VARIANT).
VARIANT).
VARIANT).
VARIANT).

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Gaps

14;

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960

AAGFSEP-GDCGGILRCEHGVIGLVTMGG

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUCS_BOVIN P98091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bhargava A.K., Woitach J.T., Davidson E.A., Bhavanandan "Cloning and cDNA sequence of a bovine submaxillary glan protein containing two distinct domains.";

Proc. Natl. Acad. Sci. U.S.A. 87:678-6802(1990).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: SUBMAXILLARY MUCOSAE.
-!- SIMILARITY: TO PORCINE APOMUCIN.
                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01208; VWFC; 1.
PROSITE; PS01185; CTCK_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00007; Cys_knot; 1.
SMART; SM00041; CT; 1.
SMART; SM00214; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M36192; AAA30657.1; -.
InterPro; IPR000359; Cys_knot.
InterPro; IPR001007; VWE_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Submaxillary gland; MEDLINE=90370871; PubMed=2204065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria
Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submaxillary mucin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
    192
                                      21
                                                                                  Local
IQTGITGTGS----GTTSSPGGFNAEATTFKEHVRTTETRILSGTTRGRSGTTV----IP-
                                    VDNGVEGEPEIECGPTSITINFNTR-NAFEGHYYVKGLYDQEGCRNDEGGRQVAGISLPF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein. 61 15
                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01225; CTCK_2;
                                                                                                                                       158

161 71

112 122

148 158

158 404

71 555

1 282

1 518

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284

477

477

58913 MW;
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485
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148
338
471
                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33, Created)33, Last sequence update)41, Last annotation update)
                                                                                              4.18;
                                                                             33;
                                                                                                                                                     is not removed. Usage by and --- is not removed. Usage by and --- agreement (See http://www.isb-sib.ch/announce/
                                                                           Score 83.5; I
Pred. No. 12;
83; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                              DB 1;
                                                                           115;
                                                                                                                                                         CRC64;
                                                                                                                  Length 563;
                                                                             Indels
                                                                                                                                                                                            (POTENTIAL).
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gland mucin-like
                                                                                                                                                                            (POTENTIAL)
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                                                                           91;
                                                                           Gaps
243
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116

GPLGQGVAMA-VGMAMAERHLAATYNRDGYNIVDHYTYTICGDGDLMEGVSAEAASLAGH

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RESULT 20
TKT_BACHD
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                                                                                   Best Loc
Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                    InterPro: IPR000360: Transketolase.
Pfam; PF00456; transketolase; 1.
Pfam; PF02779; transket_pyr; 1.
Pfam; PF02780: transketolase_C; 1.
TIGRFAMs; TIGR00232; tk11ase_bact; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldeh 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate.
-!- CCFACTOR: THIAMINE PYROPHOSPHATE (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Transketolase (EC 2.2.1.1) (TK).
TKT OR BH2352.
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP001515; BAI
HSSP; P23254; 1TRK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9KAD7;
16-OCT-2001
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161 GPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKY 220
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                                                                                   . Similarity 23. 39; Conservative
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                                                                                                                                                                                                     666
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irama C., Nakamura Y., Ogasawara N
                                                                                                                                                                                                     Thiamine pyrophosphate; Complete pr 66 AA; 72112 MW; EF6179F4F3D84D06
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                                                                                                              4.18;
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                                                                                   Score 83; DB Pred. No. 16; Pred. No. 16; Pred. No. 16; Pred. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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vuhara S.,
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5-phosphate.
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TRESULT PROBLEM OCCURS OF THE PROBLEM OCCURS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Muraki A., Muraki A.,
RA Kohara M., Matsumoto M., Muraki A., Muraki A.,
RA Kohara M., Matsumoto M., Muraki A., Muraki A.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Kohara M., Matsumoto M., Muraki A., Muraki A.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C.,
RA Watanabe A., Yamada M., Sato S., Takeuchi C.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
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RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Zimmermann W.,
RA Lamgham S.-A., McCullagh B., Robben J., Crymonprez B., Zimmermann W.,
RA Langham S.-A., McCullagh B., Robben J., Crymonprez B., Zimmermann W.,
RA Katerem M., Dirkse W., Mooljana P., Klein Lankhorst R.,
RA Waltzeneger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Kirchoff M., Lamberth S., Villarroel R.,
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                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphodiesteric bond.
-I- CATALYTIC ACTIVITY: A phosphatidylcholine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. Columbia;
MEDLINE-21016721; PubMed-11130714;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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15-JUN-2002 (Rel. 41, Last annotation update)
Phospholipase D zeta (EC 3.1.4.4) (AtPLDzeta)
PLDZETA OR AT5G25370 OR F18G18.110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Hydrolyzes glycerol-phospholipids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 408:823-826(2000).
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                                                                                                                              subfamily.
- SIMILARITY: (
                                                                                                                                                                                                          toward calcium can be anticipated for of two potential calcium ligands.

SIMILARITY: Belongs to the subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                       phosphatidate.
COFACTOR: Calcium (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                similarity).
DOMAIN: C2 d
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Best Local
                                                                                                                                                                 PAPA_HUMAN STANDARD; PRT; 1627 AA.

013219; 008371; 09UDK7;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Pregnancy-associated plasma protein-A precursor (EC 3.4.24.-) (PAPP-A)

(Insulin-like growth factor-dependent IGF binding protein-4 protease)

(IGF-dependent IGFBP-4 protease) (IGFBP-4ase).
 associated plasma induction by CAMP
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                                   Haaning J., Oxvig C., Sottrup-Jensen L.;
                                                                           SEQUENCE FROM N.A., TISSUE-Placenta;
                                                                                                                          Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                               NCBI_TaxID=9606
                          "Complete cDNA sequence of the
                                                               MEDLINE=96203921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 VDRAYRVQCFYMEADKTVSAQ-----IEVSEITTAFQTQIVPMPVCRY-EILDGGPTGQ
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                                                                                                                                                                                                                                                                                                                                 DRTSHEVFKRDGLMMTHD
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C., Overgaard M.T.,
                                                                                                                      Chordata;
Primates;
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Catarrhini;
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MEDLINE-95057018; PubMed-7526035;
Bonno M., Oxvig C., Kephart G.M., Wagner J
Sottrup-Jensen L., Gleich G.J.;
"Localization of pregnancy-associated plas
colocalization of pregnancy-associated pla
ribonucleic acid and eosinophil granule ma
ribonucleic acid in placenta.";
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                                                                   DEVELOPMENTAL STATE PubMed-7539791;

MEDLINE-95293954; PubMed-7539791;

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Stigbrand T., Gleich G.J., Sottrup-densen L.;

"Identification of angiotensinogen and complement the proform of eosinophil major !
proteins binding the proform of eosinophii human pregnancy serum and plasma.";
J. Biol. Chem. 270:13645-13651(1995).
-i- FUNCTION: Metalloproteinase which spectone the presence of IGF, resulting in release.
                                                                                                                                                                                                  MEDLINE=99423540; PubMed=10491647;
Overgaard M.T., Oxvig C., Christinsen M., Lawrence J.B.,
Overgaard M.T., Oxvig C., Christinsen M., Lawrence J.B.,
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protein-A and the proform of eosinophil major basic protein:
expression in human reproductive and nonreproductive tissues.";
Biol. Reprod. 61:1083-1089(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, SUBUNITS, AND ENZYME REGULATION MEDLINE=20469470; PubMed=10913121;
Overgaard M.T., Haaning J., Boldt H.B., Ol
Christiansen M., Gleich G.J., Sottrup-Jens
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protein-A.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 77-1627 FROM N.A., SEQUENCE OF 81-98; 117-126; 210-224; 466-485; 507-519; 576-593; 609-621; 718-736; 742-754; 1006-1017; 1259-1273; 1369-1374; 1389-1398; 1490-1509; 1524-1533 AND 1537-1544, VARIANT SER-944, AND TISSUE SPECIFICITY.
TISSUE-Placenta, and Serum; MEDLINE-94146014; PubMed-7508748;
                                                                                                                                              DEVELOPMENTAL STAGE.
MEDLINE=95293954; Pu
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its physiological inhibitor.";
Biol. Chem. 275:31128-31133(2000)
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L.G., Yates J.R. III, Conover C.A.;
growth factor (IGP)-dependent IGF binding protein-4
by human fibroblasts is pregnancy-associated plasma
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INDUCTION: By 8-bromoadenosine-3',5'-phosphate.

PTM: There appear to be no free cysteinyl groups

SIMILARITY: CONTAINS 4 SUSHI (SCR) DOMAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: High levels in placenta and pregnancy serum. In placenta, expressed in X cells in septa and anchoring villi, and in syncytictrophoblasts in the chorionic villi. Lower levels are found in a variety of other tissues including kidney,
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SUBUNIT: Homodimer;
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sa
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                           EMBL; AP001512; BAB05415.1; HSSP; Q52428; 1B8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     halodurans and genomic sequence comparison with Bacillus Nucleic Acids Res. 28:4317-4331(2000).
-I- CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA(Asn) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus halodurans.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Asparaginyl-trnA synthetase (EC 6.1.1.22) (Asparagine--trnA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYN_BACHD
                                                           InterPro;
                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASNS
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                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diphosphate + L-asparaginyl-tRNA(Asn).
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR BH1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPLKYKVVRDPPLQMDVASILHLNRKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPEGESMEMGLSIALIAAVIITISEKE 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      II-------DVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICM--
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  IPRO02106; AATRNA_ligaseII.
IPRO04522; ASNS.
IPRO04364; tRNA-synt_2.
IPR002312; tRNA-synt_asp.
IPR004365; tRNA_anti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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; tRNA-synt_2.
; tRNA-synt_asp.
; tRNA_anti.
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19.98;
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Pred. No.
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RESULT 24
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Best Local
                                                                                                                                                                                                                                                                                                                     DPOE HUMAN STANDARD,

DPOE HUMAN STANDARD,

Q07864; Q13533;

Q1-CCT-1994 (Rel. 30, Created)

16-CCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Cast annotation update)
                                                                                                                                                             Kesti T., Frantti H., Syvaoja J.E.;
"Molecular cloning of the cDNA for the polymerase epsilon.";
J. Biol. Chem.
                                                                                                          REVISIONS.
Syvaoja J.E.;
Submitted (JUN-1998)
                                                            SEQUENCE FROM N.A. Asahara H., Goldsmith J.S., Submitted (FEB-1996) to the
                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                            polymerase II subunit A).
POLE OR POLE1.
                        -!- CATALYTIC ACTIVITY: N
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGR00457; asnS; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1042; TRNASYNTHASP.
TIGREAMS; TIGRO0457; asnS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             367
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                                                FUNCTION:
                                   REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKKRSAEPENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKPVFITHYPTSLKPFYMEPDPNRDDV-VLCADLIAPEGYGEI-IGGS----QRISDYDL
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            DNA } (N)
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CONSISTS
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OF.
TWO
                        deoxynucleoside triphosphate = N diphosphate
                                                IN DNA
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                                                            Lee E., Linn S.;
EMBL/GenBank/DDBJ
                                                                                                              EMBL/GenBank/DDBJ
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Pred.
SUBUNITS
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No. 12;
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(258
                                                                                                                                                                                    catalytic
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IN CHROMOS
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RESULT 25
TORA_ED
TORA_E
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AC
P33225
D7 01-FEB
D7 15-JUN
DF Trimet
DE Trimet
GN TORA C
GOS Escher
OC Bacter
OC Escher
OC Escher
OC MacTen
RA NCBLIN
RP SEQUEN
RP SEQUEN
RP SEQUEN
RA MEDLIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trimethylamine-N-oxide-reductase precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1076
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                                                                                                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                reductase 1) (Trimethylamine oxidase 1).
TORA OR 80997.
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P33225; P78227;
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SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:9177; POLE. MIM; 174762; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                             Mejean V., 1
Pascal M.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                          MEDLINE=94293785; PubMed=8022286;
                                                                                                                                SEQUENCE
                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                             Escherichia.
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DOMAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE NOTERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR COMPLEXING SUBUNITS B AND C. THE C-TERMINUS MAY ALSO REGULATE THE CATALYTIC ACTIVITIES OF THE ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE CATALYTIC ACTIVITIES OF THE ENZYME.
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. HIGH
SIMILARITY WITH FUNGAL DNA POLYMERASE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAEPENI
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                                                                                                                             FROM N.A.,
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2286 AA;
                                                  Iobbi-Nivol C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ); DNA-directed DNA polymerase; ; Zinc-finger; Nuclear protein 2158 2190 C4-TYPE (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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  respiration
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                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                gamma subdivision;
                                                Lepelletier M., Giordano G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
  in
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clear protein.
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
MW; A216FELEAD137DEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
  Escherichia coli: involvement of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                   Enterobacteriaceae;
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EMBL; AE000201; AAC74082.1; -.
EMBL; D90736; BAA36139.1; -.
EMBL; D90737; BAA35764.1; -.
EMBL; D16500; -; NOT_ANNOTATED_CDS.
PIR; S34222; S34222.
HSSP; 087948; ITMO.
ECOGene; EG11814; TOTA.
                                                                      CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12 / MG1655;

MEDLINE-97456617; Pubmed-9278503;

Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl

Blatther F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D

Mau B., Shao Y.;

Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region
                                                        SIGNAL
                                                                                                                                                                                                                                                                                                    EMBL; X73888; CAA52095.1; -.
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ueguchi C., Kakeda M., Yamada H., Mizuno T.;
"An analogue of the DnaJ molecular chaperone in
Proc. Natl. Acad. Sci. U.S.A. 91:1054-1058(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 767-848 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 3:137-155(1996).
[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: Molybdenum (Molybdopterin) (By SUBUNIT: Interacts with the N-terminal de SUBCELLULAR LOCATION: Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c. Nati. Acad. Sci. U.S.A. 91:1054-1058(1994). FUNCTION: Reduces trimethylamine-N-oxide (TMAO) trimethylamine; an anaerobic reaction coupled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: NADH + trimethylamine-N-oxide = NAD(+) trimethylamine + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXIDOREDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE PROKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence nce 277:1453-1474(1997).
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                                                                    proteome.
 40
173
176
256
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173
176
256
TRIMETHYLAMINE-N-OXIDE
L -> R (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
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n on the lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
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lyhew G.F.
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RX MEDLINE=20365717; PubMed=10910347;
RX MEDLINE=20365717; PubMed=10910347;
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marsino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matskuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menck C.F.M., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Menck C.F.M., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Menck C.S., Pereira G.A.G., Pereira H.A. Jr., Persis A.,
RA Menck C.S., Sonterlo P.G., Rodrigues V., de Rosa A.J.M.,
RA Menck C.S., de Sa R.G., Santeril D.A., Paris A.,
RA Menck C.S., de Sa R.G., Santeril D.A., Paris A.,
RA Menck C.S., de Sa R.G., Santeril R.V., Sawasaki H.E.,
RA Gensa V.E. Jr., de Sa R.G., Santerili R.V., Sawasaki H.E.,
RA de Rosa V.E., Jr., de Sa R.G., Santerili R.V., Sawasaki H.E.,
RA de Rosa V.E., Tr., de Sa R.G., Santerili R.V., Sawasaki H.E.,
RA de Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
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15-UN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carbamoyl-phosphate synthase large chain (EC phosphate synthase large chain (EC CARB OR XF1107.
Xylella fastidiosa.
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T -> S (IN REF. 1).
KL -> NV (IN REF. 1).
QQ -> HE (IN REF. 1).
L -> M (IN REF. 1).
P -> L (IN REF. 1).
P -> L (IN REF. 1 AND 3).
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InterPro; IPRO05479; CPase_L_D2.
InterPro; IPRO05480; CPase_L_D3.
InterPro; IPRO05481; CPase_L_N.
InterPro; IPRO04362; MGS_like.
Pfam; PF002786; CPSase_L_chain; 2.
Pfam; PF002787; CPSase_L_D2; 2.
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PROSITE; PS00867; CPSASE_2; 2.
Arginine biosynthesis; Pyrimidine biosynthesis;
                                  190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence of the plant pathogen xylella fastidios nature 406:131-159(2000).
-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)0 phosphate + L-glutamate + carbamoyl phosphate.
-!- COPACTOR: Binds three manganese ions (By similarity).
                                                                                                                                          101
                                                                                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entitles requires a license agreement (sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                      50 GHYYVKGLYDQ--EGCRNDE-----GGRQVAGISLPFDSCNVARTRSLNPRGIFVTTT 100
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GYPLVVRPSYVLGGRAMEIVYGEADLARYVRDAVKVSNDSPVLLDRFLDNAVEVDVDIIA
                                                                                                                                      VVISFHPLFV-TKVDRAYRVQCFYMEADKTVSAQIEVSEI-----
                                                                                                                                                             GTAYLYSTYEEECEAAPSDRRKIMILGGGPNRIGQGIEFDYCCVHAALALREDGF---ET
                          -FCAVVHSCFVDDGNG-------DTVEILNADGCALDKYLLNNLEYPTDLMA
                                                                            AFQTQIVPMPVCRYEILDGGPTGQPVQFAI----IGQPVYHKWTCDSETVDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Arginine biosynthesis; first step.
PATHWAY: Pyrimidine biosynthesis; first step.
SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used the large (or ammonia) chain to synthesize carbamoyl phosphate
                                                    ALEANGVPVIGTSPESIDLAEDRERFQKLVQQLGLRQPP----NCTARTAEEALVLAREI
                                                                                                        IMVNCNPETVSTDYDTSDRL---YFE-PLTLEDVLEIVEVEHPVGVIVQYGGQTPLKLAK 652
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P00968; 1A9X
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CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
OLIGOMERIZATION DOMAIN.
CARBAMOYL PHOSPHATE SYNTHETIC DOMA
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MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

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MANGANESE 3 (BY SIMILARITY).

MANGANESE 3 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                    143;
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MOUSE
CO3_MOUSE
                                     Cancer
[7]
                                                 SEQUENCE OF 25-41 AND 749-760.

SEQUENCE OF 25-41 AND 749-760.

MEDLINE=93373334; PubMed=8364938;

Hamada J.-I., Cavanaugh P.G., Miki K., Nicolson G.L.;

"A paracrine migration stimulating factor for metastatic secreted by mouse hepatic sinusoidal endothelial cells: identification as complement component C3b.";

Cancer Res. 53:4418-4423(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 658-761 FROM N.A.
MEDLINE-84201365; PubMed-6609661;
Fey G.H., Wiebauer K., Dondey H.;
"Amino acid sequences of mouse complement
sequences of cloned cDNA.";
Ann. N.Y. Acad. Sci. 421:307-312(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wetsel R.A., Lundwall A., Davidson F., Gibson T., Tack B.F., Fey G.H. "Structure of murine complement component C3. II. Nucleotide sequence of cloned complementary DNA coding for the alpha chain."; J. Biol. Chem. 259:13857-13862(1984).
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01-FEB-1996 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement C3 precursor (HSE-MSF) [Contains: C3A anaphylatoxin].
                                                                                                                                                                                                                                                                                                           Wiebauer K., Domdey H., Diggelmann H., "Isolation and analysis of genomic DNA component of mouse complement.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        component of mouse complement.";
Proc. Natl. Acad. Sci. U.S.A. 79:7619-7623(1982).
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MEDLINE=85054819; PubMed=6094532;
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21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-34 FROM N.A. MEDLINE=83117622; PubMed=6985486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domdey H., Wiebauer K., Kazmaier M.,
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     ALTERNATIVE
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m FV}
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Sciurognathi; Muridae;
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Prodom; PD003264; ANAPHYLATOXIN; 1.

SMART; SM00104; ANATO; 1.

PROSITE; PS00477; ALPHA_2_MACROGIOBULIN;

PROSITE; PS01177; ANAPHYLATOXIN_1; 1.

PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                                                                                                  Pfam; PF00207; A2M; 1.
Pfam; PF01759; NTR; 1.
Pfam; PF01821; ANATO; 1.
Pfam; PF01835; A2M_N; 1.
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EMBL; J00369; AAAA77336.1; -.
EMBL; J00367; AAAA37336.1; JOINED.
EMBL; M3032; AAAA37378.1; -.
EMBL; Z37998; CAA86099.2; -.
EMBL; Z37998; CAA86099.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as 1049 we by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cahen-Kramer Y., Martensson I.L., Melchers F.;
"The structure of an alternate form of complement C3 that displays costinulatory growth factor activity for B lymphocytes.";
J. Exp. Med. 180:2079-2088(1994)
-i- FÜNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTR REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR001840; Anaphylatoxn.
InterPro; IPR00159; MacrogloblnA2.
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                   Inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRÓDUCTS: 2 isoforms; a long form (shown h short form; are produced by alternative initiation. MISCELLANDOUS: C3B IS RAPIDLY SPLIT IN TWO POSITIONS B AND A COFACTOR TO FORM IC3B (INACTIVATED C3B) AND C3F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3, C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. I INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES. THE SHORT ISOFORM HAS B-CELL STIMULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN. SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain, releasing C3A anaphylatoxin and generating C3B (beta chain + alpha' chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: C3 precursor is first processed by the removal of 4 arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO FORM C3C AN
AS C3D OR C3G.
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                                                                                                                                  Complement alternate pathway; Plasma; se; Glycoprotein; Signal; Alternative
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             COMPLEMENT C3. BETA COMPLEMENT C3, ALPH COMPLEMENT C3, SHOR FOR SHORT ISOFORM. C3A ANAPHYLATOXIN.
                                                    ALPHA
SHORT
                                                                                     BETA CHAIN
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Matches 65
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                                                       STRAIN-Bristol Wilkinson J.;
Submitted (NOV-
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INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC...).

N-LINKED (GLCNAC...).
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C3G FRAGMENT.
C3D FRAGMENT.
C3F FRAGMENT.
C1EAVAGE (BY C3 CONVERTASE).
CLEAVAGE (BY FACTOR I).
CLEAVAGE (BY FACTOR I).
                                                       EMBL/GenBank/DDBJ databases
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InterPro; IPR001813; 60s_ribosomal.
InterPro; IPR001790; Ribosomal_L10.
Pfam; PF00428; 60s_ribosomal; 1.
Pfam; PF00466; Ribosomal_L10; 1.
SEQUENCE FROM N.A.
STRAIN-Mu50 / ATCC 700699, and N315;
STRAIN8-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuza Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian Kanamori M., Matsumaru H., Maruyama A., Muraka Mizutani-Ui Y., Takahashi N.K., Sawano T., Ino
                                                                                                                                                                                                          Staphylococcus aureus (strain Mu5)
Staphylococcus aureus (strain N31)
Bacteria; Firmioutes; Bacillales;
BCBI_TaxID-158878, 158879;
                                                                                                                                                                                                                                                                                                                                                            SYN_STAAM STANDARD; PRT; 430 AA 099U35; 099U35; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Asparaginyl-trna synthetase (EC 6.1.1.22) (Asparaginyl-trna synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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Bini L., Heid H., Liberatori S., Geier G., Pallini V.,
"Two-dimensional gel electrophoresis of Caenorhabditis homogenates and identification of protein spots by micr electrophoresis 18:557-562(1997).

-- FUNCTION: RIBOSOMAL PROTEIN PO IS THE FUNCTIONAL EQ OF E.COLI PROTEIN LIO.

-- SUBUNIT: PO FORMS A PENTAMERIC COMPLEX BY INTERACTI DIMERS OF P1 AND P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein; Phosphorylation.
INIT_MET 0 0
SEQUENCE 311 AA; 33642 MW; 2FA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               ASNS OR SAV1454 OR SA1287.
                                                                                                                                                                                                                                                                                                                                            (AsnRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EITTAFQTQIVPMPVCR--YEIL-----DGGPTG-------QPVQFAIIGQPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNN------LE
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Pred. No. 9
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N315)
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                                                                                                                                                                                                                                                                                                                                                              update)
.22) (Asparagine--tRNA
     T., Yuzawa H., K
., Lian J.-Q., I
, Murakami H., H
T., Inoue R.-I.
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       Hosoyama
I., Kaito
                                                     Kobayashi
Ito T.,
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                          P14856;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation updat
Seed lipoxygenase-2 (EC 1.13.11.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Sh. Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002312; tRNA-synt_i
InterPro; IPR004365; tRNA_anti.
Pfam; PF00152; tRNA-synt_2; 1.
Pfam; PF01336; tRNA_anti; 1.
PRINTS; PR01042; TRNASYNTHASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA(Asn) = AMP + diphosphate + L-asparaginyl-trNa(Asn).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGR00457; asnS; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP003362; BAB57616.1; -. EMBL; AP003133; BAB42547.1; -. HSSP; Q52428; 1B8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                 PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR004522; AsnS.
InterPro; IPR004364; tRNA-synt_2.
                                                                                                                                             LOX2_PEA
                                                                                                                                                                                                                                  388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 VISFHPLFVTKVDRAYR--VQCFYMEADKTVSAQIEVSEITTAFQTQIVP--MPVCRYEI 157
                                                                                                                                                                                                                                  RRYGSVPH-----C---
                                                                                                                                                                                                                                                                  RHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIALIAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFSFGPTFRAEKSKTRRHLIEFWMIEGEMAFTNHAESLEIQEQYVTHVVKSVLENCKLEL
                                                                                                                                                                                                                                                                                                    IAPEGYGEI-IGGS----ERVDDLELLEQRVKEH--
                                                                                                                                                                                                                                                                                                                                     --PQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQALPVDL 330
                                                                                                                                                                                                                                                                                                                                                                         ----FDDIEWGEDFGAPHETAIANHYDLPVFITNYPTKIKPFYMQPNPENEETVLCADL
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55; Conser
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                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.0%;
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tRNA-synt_asp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80.5;
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                                                                                                                                               864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 430;
                                                                                                                                                                                                                                                                    373
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EMBL; X78580; CAA55318.1; -.
PIR; S07075; S07075.
HSSP; P08170; 2SBL.
InterPro; IPR000907; Lipoxygenase.
InterPro; IPR001024; Lipoxygenase_LH2.
Pfam; PF00305; Iipoxygenase; 1.
Pfam; PF01477; PLAT; 1.
                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casey R.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PLANT LIPOXYGENASE MAY BE INVOLVED IN A NUMBER OF DIVERSE ASPECTS OF PLANT PHYSIOLOGY INCLUDING GROWTH AND DEVELOPMENT, PEST RESISTANCE, AND SENESCENCE OR RESPONSES TO WOUNDING. IT CATALYZES THE HYDROPEROXIDATION OF LIPIDS, CONTA A CIS, CIS-1,4-PENTADIENE STRUCTURE.

-I- CATALYTIC ACTIVITY: Linoleate + O(2) - (92,11E)-(13S)-13-hydroperoxyoctadeca-9,11-dienoate.
-I- COFACTOR: IRON.
                                                                                                                                                                                                                                                                                            METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum. NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00081; LIPOXYGENASE_2;
PROSITE; PS00711; LIPOXYGENASE_1;
                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00087; LIPOX SMART; SM00308; LH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 264:929-932(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The cDNA cloning of a pea (Pisum Sequence comparisons of the two ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ealing P.M., Casey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Birte;
MEDLINE=90147555; PubMed=2515855;
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362
                                                                                                                                      36
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY
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                                                                                                                                     TSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGI 95
                         EILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFV-
                                                                              FVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRY 155
                                                                                                             SAFDLNF-TPNEFDSFQDVRNLFE------GGIKLPLD----
                                                                                                                                                                                Similarity
                                                      -VISTLSPLPVVK---
                                                                                                                                                                                                                        864 AA;
                                                                                                                                                                                                                                     529
716
864
333
562
578
                                                                                                                                                                  Conservative
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18.3%;

    KSAWMTDEEFAREMLAGVNPCMIRGLQEFPPKSNLDPAE

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MISSING (IN REF. 2).
L -> I (IN REF. 2).
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                  EMBL; AE005293; AAG55544.1; -.
EMBL; AP002554; BAB34575.1; -.
InterPro; IPR001467; Prok_Mboxred.
Pfam; PF00384; molybdopterin; 1.
Pfam; PF01568; Molydop_binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-0157:H7 / RIMD 0509952;

STRAIN-021156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohakayama K., Murata T., Tanaka M., Tobe T iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H., Scherichia coli 0157:H7 and genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001)

--- FUNCTION: Reduces trimethylamine-N-oxide (TMAO) into
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15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kirk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V
                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outs
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Periplasmic (By SIMILARITY: BELONGS TO THE PROKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trimethylamine + H(2)0 COFACTOR: Molybdenum ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
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                                                                                                                                                                                   an email to license@isb-sib.ch).
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
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Best Local
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                                                                                                                               MEDLINE-94193805; PubMed-8144680;
Yun H.Y., Keutmann H.T., Eipper B.A.;
"Alternative splicing governs sulfation of tyrosine or on peptidylycine alpha-amidating monooxygenase.";
J. Biol. Chem. 269:10946-10955(1994).
-I-FUNCTION: C-terminal alpha-amidation of peptides. To produces a peptidyl(2-hydroxyglycine) intermediate of dismutates to glyoxylate and the corresponding desg
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Peptidyl-glycine alpha-amidating monooxygen
(EC 1.14.17.3) (PAM).
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SIGNAL
                                                                                                                                                                                                                                                         Biochem.
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                                                                                                                                                                                                                                   SULFATION
                                                                                                                                                                                                                                                        "Ruman peptidylglyche alpha-amidating monooxygenase: cDNA, c."Human peptidylglyche alpha-amidating monooxygenase: cDNA, c. and functional expression of a truncated form in COS cells."; Biochem. Biophys. Res. Commun. 169:551-558(1990).
                                                                                                                                                                                                                                                                                                          TISSUE=Thyroid carcinoma; MEDLINE=90290494; PubMed=
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Mammalia; 1
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                                                                                        peptidyl(2-hydroxyglycine) + de
COFACTOR: COPPER AND ASCORBATE.
                                                         SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
                                               MONOOXYGENASE FAMILY.
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                                                                                                                                                                                                                                                                                                       PubMed=2357221;
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Primates;
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TRIMETHYLAMINE-N-OXIDE REDUCTASE; ABFFD02ED178932F CRC64;
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Catarrhini;
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                                                          ASCORBATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                               precursor
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                                                                                                                                                         reaction
                                                                                                                                              unstable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                                                                                                                                cloning
                                                                                                                                 peptide
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RESULT 33
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01082; Cu2_monooxygen; Pfam; PF01436; NHL; 4. Pfam; PF03712; Cu2_monoox_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M37721; AAA36414.1; -. PIR; A35477; URHUAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               culties requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
PROSITE; PS00085; CU2_MONOOXYGENASE_2; 1.
Oxidoreductase; Monooxygenase; Copper; Vitamin C; Transmembrane; Glycoprotein; Phosphorylation; Sulfation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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InterPro; IPR000720; Pamonoxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000323; Cu2_monooxygnse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 170270;
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                                                                                                                                                                                                                                                                                                                CGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLPFDSCNVARTRSLNP
                                                            AVIITISFK 380
                                                                                PTSSELQKMQEKQKLIKE
                                                                                                    TDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIALIA 371
                                                                                                                                            QISITIKEPNSECV-RPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVR
                                                                                                                                                                  -----VMNFSNGEIIDIF-----KPVRKHFDMPHDIVASEDGTVY
                                                                                                                                                                                                                              QIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCA 192
                                                                                                                                                                                                                                                   SGKFITQWGEESSGSSPLPGQFTVPHSLALVPLLGQLCVADRENGRIQCFKTDTKEFVRE
                                                                                                                                                                                                                                                                                               CQPTDVAVDPGT-----GAIYVSDGY-----
                                         AIAIFIRWK
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                                                                                                                                                                                                                                                                          RGIFVTT----
                                                                                                                                                                                                                                                                                                                                        66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00790; PAMONOXGNASE
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                         --IGDAHTNTVWKFTLTEKLEHRSVKKAG
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                                                                                                                                                                                                                                                                        TV--VISFHPLF--VTKVDRAY-RVQCFYMEADKTVSA 132
                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (PC MW; E9FD60AF3402B0B5 CRC64;
                                                                                                                                                                                                                                                                                                                                      Score 80; DB:
Pred. No. 50;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                COPPER
COPPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTRAGRANULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MONOOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDYL-GLYCINE ALPHA-AMIDATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROBABLE.
                                                                                                                                                                                                          -------GLLFAVNGKPHFG----DQEPVQGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                         R (POTENTIAL).
R (POTENTIAL).
R (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                      115;
                                                                                                                                                                                                                                                                                                                                                          Length 974;
                                                                                                                                                                                                                                                                                                                                      Indels 130;
                                                                                 TTTLLVIPVVVLL
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Best Local 9
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Smith D.R., Doucette-Stamm L.A., Deloughery C:, Lee H.-M., Dubois Smith D.R., Doucette-Stamm L.A., Deloughery C:, Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Rarrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Paniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
(AdSS) (AMPSase).
                                                                                                                                                                                                                                                                                            NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PURA_METTH 026712;
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                       PROSITE; PS01266; ADEXYLOSUCCIN_SYN_1; FALSE_NEG.
PROSITE; PS00513; ADENYLOSUCCIN_SYN_2; FALSE_NEG.
PUTINE biosynthesis; Ligase; GTP-binding; Complete
NP_BIND 12 18 GTP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000843; AAB85121.1; -. HSSP; P12283; 1ADE.
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Methanobacteriaceae; Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PURA OR MTH615
                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001188; Asucc_synthtase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00709; Adenylsucc_synt;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum
 165
                                   324
                                                                    112
                                                                                                                                                                        205
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                                                                                                                                      64
                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenylosuccinate.
PATHWAY: AMP biosynthesis; first committed step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE BIOSYNTHESIS.

CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP +
 EAL-
                               QALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGESMFMG
                                                                   EQDQSSSYLSKKIGSTGTG----CGPANAERVMRTAKLAREVEELGDFLTDV-PLEV---N
                                                                                    ECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDN 323
                                                                                                                                  EDARLLIGAGVLVDPEVFLHEMEYLSK-----
                                                                                                                                                                      DTVEILNADGCALD-KYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNS
                                                                                                                                                                                                         39;
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                               TIGR00184; purA; 1
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340 AA;
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---DEGEDVFVEGSQG-----
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; 37205 MW;
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                                                                                                                                                                                                       26;
                                                                                                                                                                                                                      Score 79.5;
Pred. No. 14;
                                                                                                                                                                                                                                                                         BY SIMILARITY.
; 5726F32397F16B07 CRC64;
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 -FGLSLYYG
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 188
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YEW2\_YEAST

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RESULT 35
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Best Local :
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--- SIMILARITY: TO S.POMBE RALZ.
                                                                                                                 1156
                                                                                                                                                                                                                                                                                      1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Wei Y., Ta
Submitted
                                                                                                                                                                                                                                 1062
                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 1753 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U18916; AACO3230.1; PIR; S30855; S30855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Mulligan J.T., Die Wei Y., Taylor P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycesae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequ
01-FEB-1995 (Rel. 31, Last anno
Hypothetical 195.4 kDa protein
YER132C OR SYGP-ORF50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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P32634;
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                                                        SESYQDTLEIKRSLANIDNGYVDSYLLRNTS-----MAQSIH--
                                                                                                                                                                                               TVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILD
                                                                                                                                                                                                                           KEGEFFSSKSYINNEKSRRLSYISNPE---SVESTNSNNNAIIELEPLLTPRSLYMPWST
                                                                                                                                                                                                                                                                                                   GGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCF-----VDDGNG------
                                                                                                                                                                         ASVRAFAEFFYT - - - - -
                                                                                                                                                                                                                                           LLSNSYGSDIPYEASIQEYGMNNGRDEEEDGDNQDYGCISPSNIRPIFSTINAININGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                             S0000934; PMD1.
                                                                                                                                                                                                                                                                                                                                                                                                                               PF01344; Kelch;
                                                                                                                                                                                                                                                                                                                                             l Similarity
63; Conserv
                                                                                  DTVEI----LNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.T., Dietrich F.S., Hennessey K.M., Sehl P., |
aylor P., Nakahara K., Roberts D., Davis R.W.,
(FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                              PILYELITEVLYKIISKKEEGLSVTCEALLNLFQQKVSRYCNENEGKIRKQLDS
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                         3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelch.
                                                                                                                                                                                                                                                                                                                                                                                                     195382
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1.2e+02;
hes 94;
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Cherry J.M.,
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MEDLINE-87286375; PubMed-3039294;
Souciet J.-L., Potier S., Hubert J.-C., Lacroute F.;
"Nucleotide sequence of the pyrimidine specific carbamoyl phosphate synthetase, a part of the yeast multifunctional protein encoded by the URA2 gene.";
                                                                                                                                                                                                                                                                                          Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.; "Sequence analysis of a 40.7 kb segment from the left arm chromosome X reveals 14 known genes and 13 new open readin including homologues of genes clustered on the right arm o chromosome XI.";
Yeast 12:787-797(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;
"Sequencing analysis of a 40.2 kb fragment of yeast chromosome reveals 19 open reading frames including URA2 (5' end), TRK1, F SPT10, GCD14, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA gen three remnant delta elements and a Ty4 transposon.";
Yeast 12:1471-1474(1996).
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288c / FY1679; MEDLINE=96408771; PubMed=8813765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast
[5]
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STRAIN-ATCC 28583 / FL100;
MEDLINE-89378778; PubMed-2570735;
MEDLINE-89378778, PubMed-2570735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of the aspartate transcarbamylase region of the URA2 gene product in Saccharomyces cerevisiae. Features involved in activity and nuclear localization.";
J. Biol. Chem. 264:8366-8374(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89255278; PubMed-2498313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Souciet J.-L., Nagy M., le Gouar M., Lacroute F., Potier S.; "Organization of the yeast URA2 gene: identification of a defective dihydrocrotase-like domain in the multifunctional carbamoylphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 175-2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase-aspartate transcarbamylase complex."; Gene 79:59-70(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URA1 protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase (EC 6.3.5.5); Aspartate carbamoyltransferase (EC 2.1.3. URA2 OR YJL130C OR J0686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1988 (Rel. 07,
01-NOV-1995 (Rel. 32,
15-JUN-2002 (Rel. 41,
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
+ N-Carbamoyl-L-aspartate.

PATHWAX: Pyrimidine biosynthesis; first step.

PATHWAY: Pyrimidine biosynthesis; second step.

PATHWAY: Pyrimidine biosynthesis; second step.

PATHWAY: Pyrimidine biosynthesis; second step.

MISCELLANEOUS: GATASE (GLUTAMINE AMIDOTRANSFERASE) AND CPSASE (CARBAMOYL PHOSPHATE SYNTHASE) FORM TOGETHER THE GLUTAMINE-DEPENDENT CPSASE (GD-CPSASE) (EC 6.3.5.5).

MISCELLANEOUS: IN EUKARYOTES EC 6.3.5.5 IS SYNTHESIZED BY TWO PATHWAY-SPECIFIC (ARGININE AND PYRIMIDINE) UNDER SEPARATE CONTROL.

SIMILARITY: THE CPSASE DOMAIN IS SIMILAR TO OTHER CPASES.

SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE DHOASE FAMILY.
                                                                                                                                                                              AND ATCASE).

CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + phosphate + glutamate + carbamoyl phosphate.

CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspart
                                                                                                                                                                                                                                                                           FUNCTION: THIS
                                                                                                                                                                                                                                                            ENZYMATIC ACTIVITIES
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Last annotation update)
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the right arm of
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PRINTS; PRO0100; AOTCASE.

PRINTS; PRO0098; CPSASE.

PRINTS; PRO0099; CPSGATASE.

PRINTS; PRO0096; GATASE.

PRINTS; PRO0096; GATASE.

TIGREAMS; TIGRO0670; asp_carb_tr; 1.

PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.

PROSITE; PS00442; GATASE_TYPE_I; 1.

PROSITE; PS00442; GATASE_TYPE_I; 1.

PROSITE; PS00867; CPSASE_1; 2.

PROSITE; PS00867; CPSASE_2; 2.
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HSSP;
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EMBL; X05553; CAA29068.1; -.
EMBL; J04711; AAA35198.1; -.
EMBL; Z49405; CAA689425.1; -.
EMBL; X87371; CAA60825.1; -.
EMBL; D28139; BAA05680.1; -.
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n; PF00185; OTCAGE; 1.
n; PF00289; CPSASE_L_Chain; 2.
n; PF00744; Dihydroorotase; 1.
n; PF00988; CPSASE_Sm_Chain; 1.
n; PF02142; MGS; 1.
n; PF02729; OTCAGE(N; 1.
n; PF02729; OTCAGE(N; 1.
n; PF02787; CPSASE_L_D2; 3.
m; PF02787; CPSASE_L_D3; 1.
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SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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; P00968; 1A9X.
S0003666; URA2.
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IPR002082; Asp_carbmltransf.
IPR001317; CPS_GATase.
IPR000901; CPSase.
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IPR000991; GATase_1.
IPR004362; MGS_1ike.
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     biosynthesis; Ligase;
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ELKVVPWN -> RIESCSMD (IN REF. 1 A

I -> Y (IN REF. 1 AND 2).

GA -> VQ (IN REF. 1 AND 2).

GI -> RF (IN REF. 1 AND 2).

GI -> RF (IN REF. 1 AND 2).

RDTEFLEDV -> EIQNSCLT (IN REF. 1

KAH -> QGT (IN REF. 2).

I -> Y (IN REF. 2).

I -> N (IN REF. 2).

A -> G (IN REF. 2).

A -> G (IN REF. 2).

D -> V (IN REF. 1 AND 3).

EV -> S (IN REF. 1 AND 3).

I -> M (IN REF. 1 AND 3).
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ASE (GLUTAMINE AMIDOTRANSFERASE).
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A (IN REF. 1 AND 2).
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RESULT 36
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Best Local S
Matches 70
                                                           STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-9637999; PubMed-8880807;

Bult C.J., White O., Olsen G.J., Zhoù L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

'Complete genome sequence of the methanogenic archaeon, Methanococcus Science 372 122
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                                     Science 273:1058-1073(1996).
-!- SIMILARITY: TO M.JANNASCHII MJ0795 AND MJ1506.
                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanocaldococcaceae; Me
                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1561.
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SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
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01-NOV-1995 (Rel. 32, Created)
16-CCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                           Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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                            Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                        "The Mycobacterium leprae genome: systematic sequence analysis identifies key catabolic enzymes, ATP-dependent transport systems a novel polA locus associated with genomic variability."; mol. Microbiol. 16:909-919(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Corynebacterineae; NCBI_TaxID=1769;
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Massive gene decay in the leprosy bacillus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01047; HMA_1; 1. PROSITE; PS50846; HMA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; PF00702; Hydrolase; 1.
pRINTS; pR00119; CATATPASE.
pRINTS; PR00943; CUATPASE_E_E_
pROSITE; PS00154; ATPASE_E1_E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:1007-1011(2001).

-i: CATALTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
-i: SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES
(E1-E2 ATPASES). SUBFAMILY IB.
-i- SIMILARITY: CONTAINS 1 HMA DOMAIN.
                                                                                                                                                                                                                                         CONFLICT
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 358
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                                                                                                                           188
                                                                                                                                               478
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 GFSMFMGLSIALIAAVIITI
                                        PENIIDVRTDINTLEISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSP---
                                                                                SQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGG--AAAKPAAAAQLRLLKKRSAE
                                                                                                                          DTFCAVVHSCFVDDG---NGDTVEILNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYADR
                                                                                                                                               VEAASEHSVATAIVAAYADPRPVADFVAFAGCGVSGVVAEHHVKIGKP---SWV---
                                                                                                      NAPCDVVLESARREGESRGETVVFVSVDGVA-----
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                                                                                                                                                                                      63;
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001757; ATPase_E1-E2.
IPR001756; Cu_ATPase.
IPR001934; HeavyMe_transpt.
IPR001454; Hlgnase/hydrlase.
                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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                  -GIDTV-IADMLPEAKVDVIQR--LRDQGHTV--AMVGDGINDGPALACADL
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                                          - - <del>-</del> E
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RESULT
CADH_MC
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                                                                  Signal;
                                                                                                                                                                                                                                                                                                                                                    This SWI
between
                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no results by non-profit institutions as long as its content modified and this statement is not removed. Usage by an end of this statement is not removed.
                                                                                                                                                                  MGD; MGI:1095414; Cdh17.
InterPro; IPR002126; Cadherin.
Pfam; PF00028; Cadherin; 7.
                                                                                         PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_2; 5.
Cell adhesion; Glycoprotein; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                    DOMAIN
                                                                                                                                         SMART; SM00112;
                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                            or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohnishi K., Shimizu T., Karasuyama H., Melchers "The identification of a nonclassical cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20469471; PubMed=10906147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490-509, TISSUE SPECIFICITY, AND D STRAIN-BALB/C; TISSUE-Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angres B., Kim L., Tauber R.;
"LI-cadherin gene expression during intestinal development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Swiss Webster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CADH_MOUSE
Q9R100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOL Chem. 275.31134-31144(2000).

FUNCTION: CADEERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. LI-CADHERIN MAY HAVE A ROLE IN THE MORPHOLOGICAL ORGANIZATION OF LIVER AND INTESTINE.

SUBCELLULAR LOCATION: Type I membrane protein (Potential).

TISSUE SPECIFICITY: HIGHEST EXPRESSION IS FOUND IN INTESTINE WITH LOWER EXPRESSION IN SPLEEN, BONE MARROW, LUNG AND TESTIS. NO EXPRESSION DETECTED IN LIVER, KIDNEY, HEART, BRAIN OR SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                               AGAIN IN IMMATURE AND MATURE B-CELLS. SIMILARITY: CONTAINS 7 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE. EXPRESSED IN PRECURSOR B-CELLS AND MYELOID CELLS.

DEVELOPMENTAL STAGE: EXPRESSION INCREASES IN PRO- AND PRE-B-I
CELLS, DECREASES IN LARGE AND SMALL PRE-B-II CELLS, AND INCRE
                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                             AF177669; AAD51125.1;
D87912; BAB03264.1; -
P15116; INCI.
                                                                                                                                 PR00205; CAL
                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
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808
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Last annotation update)
(Liver-intestine-cadherin)
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CADHERIN-17.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Sciurognathi; Muridae
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OPMENTAL STAGE.
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                                                                                         Calcium-binding; Repeat;
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SEQUENCE FROM N.A.

STRAIN-ATCC 8185;
STRAIN-ATCC 8185;
MEDLINE-98012987; PubMed-9352938;
MEDLINE-98012987, PubMed-9352938;
MOOTZ H.D., Marahiel M.A.;
"The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequence and biochemical characterization of functional internal adenylation domains.";
internal adenylation domains.";
J. Bacteriol. 179:6843-6850(1997).
-i- FUNCTION: ACTIVATES THE SECOND TO FOURTH AMINO ACIDS IN TYROCIDINE
-i- FUNCTION: ACTIVATES THE SECOND TO FOURTH AMINO ACIDS IN TYROCIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                           (ProA) (Proline activase); ATP-dependent phenyl (PheA) (Phenylalanine activase); ATP-dependent adenylase (D-PheA) (D-phenylalanine activase); [ATP-hydrolyzing] (EC 5.1.1.11)].
                                                                                                                                                                                                                                                                            030408;
15-JUL-1999
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DOMAIN
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                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                    Bacillus brevis
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                                                                                                                                                                                                                                                                                                                                                            264 NDPGAQYSLVNKEKLSPFPFSI 285
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91645 MW;
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Pred. No.
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DOMAIN
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                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00455; AMP_BINDING; PROSITE; PS50075; ACP_DOMAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                             178
                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), ANI METHYLATION (OPTIONAL), MISCELLANGOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLIC DECAPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-ORN-LEU), B, C, AND D, IN WHICH PHE, AT POSTTIONS 3, 4, AND TYR RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM.
SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).

PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis.
SUBUNIT: LARGE MULTIENZYME COMPLEX OF TYCA, TYCB AND TYCC.

DOMAIN: CONSISTS OF THREE MODULES, INCLUDING AN C-TERMINAL
EPIMERIZATION DOMAIN. EACH MODULE INCORPORATES ONE AMINO ACID 1
THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS
RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLATION, CONDENSATION
RESPONSIBLE FOR SUBSTRATE ADENYLATION THIOLATION, CONDENSATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
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COFACTOR: CONTAINS 3 COVALENTLY BOUND PHOSPHOPANTETHEINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 3 ACYL CARRIER DOMAINS.
QLCKAMHPQMSVMNAYGPTESSVMAT
                                                                                                                                                                                                 VQCFYMEADKTVSAQIE-VSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVY 177
                         ---ECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEIS
                                                      KDPIALRNL----IAAWECSYVVFVPSMFQAILECSTPADIRSIQAVMLGGEKLSPKLV
                                                                                  LDKYLLNNLEYPTDLMAGQEAHVYKYADRSQLFYQCQISITIKEPNS----
                                                                                                                                             HK-----WTCD----
                                                                                                                                                                      VECLYLDEEGSYSPQTENIEPIHTAAD-----LAYIIYTSGTTGRPK-----GVMVE
                                                                                                               HRGIVNSVTWNRDEFALSVRDSGTLSLSFAFDAFALTFFTLIV---SGSTV-VLMPDHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF004835; AAC45929.1; -. P14687; 1AMU.
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               Isomerase; Antibiotic biosynthesis; Phosphopantetheine;
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iss Institute of Bioinformatics
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ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
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DOMAIN 2 (PHENYLALANINE-ACTIVATING)
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RNHL_HUMAN
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Matches 57
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160 to 17 to 1
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15-JUN-2002 (Rel. 41, Last annotation update)
Ribonuclease HI large subunit (EC 3.1.26.-) (RNase
(RNase H(35)) (Ribonuclease H2) (RNase H2).
RNASEH2A OR RNASEHI OR RNHIA.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
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Frank P., Braunshofer-Reiter C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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    189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
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SIMILARITY: BELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (JUL-2001) to the EMBL/GenBank/DDBJ databases FUNCTION: DEGRADES THE RIBONUCLEOTIDE MOIETY ON RNA MOLECULES. PARTICIPATES IN DNA REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; BC011748;
; Q57599; 1E
TFCAVVHSCFVDDGNGDTVEILNADGCALD-----KYLLNNLEYPTDLMAGQEAHVYKYA 243
                                            PVPAVCRKEPCVLGVDEAGRGPVLGPMVYAICYCPLPRLADLEALKVADSKTLLESERER
                                                                                    PMP-VCRYE--IL-----DGGPTGQPVQFAIIGQPVYH-----
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l Similarity 22.7%;
57; Conservative 40
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Acad. Sci. U.S.A. 95:12872-12877(1998)
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Pred. No. 14;
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Catarrhini; Hominidae
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## ALIGNMENTS

ASCUT-1.
ASCUT-1.
ASCATIS lumbricoides (common roundworm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.

01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CUT-1-like cuticlin protein precursor.

Q93115 Q93115;

PRELIMINARY;

PRT;

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RESULT 1
Q9311
Q931
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AC Q931
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Matches 311; Conserv
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SEQUENCE
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Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Timinouni M., Bazzicalupo P.;
"cut-1-like genes of Ascaris lumbricoides.";
Gene 193:81-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U73005; AAB66646.1; -.
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
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385 AA;
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385 CU
42408 MW;
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80.2%; Pred. No. 1.5e-151;
Live 32; Mismatches 40;
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CUT-1-LIKE CUTICLIN PROTEIN.
103C6834B1D29286 CRC64;
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Best Local
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125580; AAD28743.2;
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
SMART; SM00241; ZP; 1.
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01-OCT-2000
01-MAR-2002
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Eukaryota; Metazoa; Nematoda;
Onchocercidae; Wuchereria.
NCBI_TaxID=6293;
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Last sequence update)
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Pred. No. 6.2e-144;
9; Mismatches 44;
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Best Local
O18479;
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O1-JAN-1998
O1-JAN-1998
O1-MAR-2002
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Q19707;
01-NOV-1996 (TIEMBLICEL. (
01-NOV-1996 (TIEMBLICEL. (
01-MAR-2002 (TIEMBLICEL. 2
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F22B5.3.
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Science 282:2012-2018(1998).
EMBL; 250044; CAA90355.1; .
Interpro; IPR001507; Endoglii
SMART; SM00241; ZP; 1
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
MCBI_TaxID=6239;
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LTV--FVAIFITYMIVSRMMVPSDK
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3 (TrEMBLrel.
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Pred. No. 2.7e-125;
2; Mismatches 52;
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Best Local 9
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De Giorgi C., De Luca F., Di Vito M., Lamberti F.;
Pidorgi C., De Luca F., Di Vito M., Lamberti F.;
Modulation of expression at the level of splicing of cinfective second-stage juvenile of the plant parasitic Meloidogyne artiellia.";
Meloidogyne artiellia.";
Mol. Gen. Genet. 253:589-598(1997).
EMBL; X96677; CAA65452.1;
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
F53F1.1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                             Q9XVM7
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                        SEQUENCE FROM N.A. MEDLINE-99069613;
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                                                                                                                                SEQUENCE
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                           PubMed=9851916;
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                                                                                                                                                                                             Nematoda; Chromadorea; rinae; Caenorhabditis.
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Pred. No. 2.9e-118;
Pred. No. 2.9e-138;
                                                                                       EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                    Rhabditida; Rhabditoidea;
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Best Local S
Matches 129
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096775;
01-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
Cuticlin (Fragment).
CUT-1.
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Eukaryota; Metazoa; N
Onchocercidae; Brugia
NCBI_TaxID=6279;
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SEQUENCE
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Science 282:2012-2018(1998).
EMBL; Z81088; CABD3124.1;
Interpro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1
                                                                                                                                                                                                                                                                                                                                                    "cut-1-like genes are present in the filarial nematodes Brugia pahangi and Brugia malayi and, as in other nematodes, code for components of the cuticle.";
                                                                                                                                                                                                                                                                               InterPro; IPR001507; Endoglin/CD105
SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                    Mol. Biochem. Parasitol. 10
EMBL; AJ012617; CAA10074.1;
                                                                                                                                                                                                                                                                                                                                                                                                               Devaney
                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis E.K., Hunter S.J., Devaney E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-99339397;
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 61
                                                                      Н
                                                                    CQISITVKEPDQECVRPICEDVEGGGAPVVG
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 PTGQPIQFATIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILSADGCALDKYL
                   PTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYL
                                                                                                                                                 al Similarity
122; Conserv
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14119 MW;
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                                                                                                                                             Score 662; DB 5; 1
Pred. No. 3.6e-56;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromadorea;
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annotation
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Best Local Similarity 42.2
Matches .132; Conservative
Q21540 PRELIMINARY;
Q21540;
Q1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
M142.2 protein.
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                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z49207; CAA89068.1; -.
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
SEQUENCE 290 AA; 33215 MW; E70C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cottage
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RESULT Q19053
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Best Local (
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PFAM: PF00093; VWFADOMAIN.
PRINTS; PR00453; VWA; 1.
SMART; SM00327; VWA; 1.
SWART; SM00241; ZP; 1.
SPOSITE; PS50234; VWFA; 1.
SPOTENCE 550 AA; 61445 MW;
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Q19053;
Q19053;
O1-NOV-1996 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                              Eukaryota; Metazoa; Nemat. Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                           SEQUENCE FROM N.A. McMurray A.A.; Submitted (OCT-199
                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                            E04D5.3 protein. E04D5.3.
  SEQUENCE FROM N.A
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EMBL; Z73428; CAA97806.1; -.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR002035; VWF_A.
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PQNCKKLPGEDGHHHHHHPEKRRKLVRRLADGVGTIDVFTDSVTV
                                                                                                                                                                                Nematoda;
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                                                                                                                                                       cda; Chromadorea;
Caenorhabditis.
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                                         EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
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Pred. No. 1.4e
48; Mismatches
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                                                                                                                                                                              Rhabditida;
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Best Local :
                                                                                                                                                                    Query Match
Best Local Similarity
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Q93532;
01-FEB-1997 (TrEMBLrel. 0:
01-FEB-1997 (TrEMBLrel. 0:
01-MAR-2002 (TrEMBLrel. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z66496; CAA91280.1; -.
InterPro: IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
SEQUENCE 484 AA; 53325 MW; DD673
                                                                                                                                                                                                                                                              investigating biology.", Science 282:2012-2018(1998). EMBL; Z78542; CAB01742.1; -. InterPro; IPR001507; Endoglin/CD105. SMART; SM00241; ZP; 1.
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1996)
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                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform
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RNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFY 123
                                            RIPLFCK----YHAEQIDNGLQGEPLIRCGSESLSINFKTQGAFEGHVYVKGHYSMKHC 84
                                                                                                                                                                                                                                             315 AA;
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53325 MW; DD6737B60D7F7F3B CRC64;
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                                                                                                                                                47;
                                                                                                                                         Score 578.5; DB 5;
Pred. No. 1.4e-47;
47; Mismatches 76;
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Science 282:2012-2018(1998).
EMBL; 266565; CAA91480.1; -
InterPro; IPRO01507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      none;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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                                                                                                         WTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDL-MAGQEAH
                                                                                                                                                                                         VDYSTKDQFGRPVGGIKLNHGACNMDRQRMIAPEGMMFSTVLIISFHPLFLTRMDKAYHI
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TFKPKDAD--
                                                           VYKYADRSQLFYQCQISITIKEPNSEC---VRPQCSEPQGFGAVKTGGAAAKPAAAAQLR
                                                                                           WQCDSE----DYGLLVHSCYVEDGQGEKQMIIDERGCHTDRLLLGDPTYVEALNMAYRESF
                                                                                                                                      RCMYKEAARTVTAAIDVSNLPTESVQSDLPMPTCSYTIRRDQLDGPILKYAKVGDQVVHR
                                                                                                                                                                QCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHK
                                                                                                                                                                                                                ----NDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRV 119
                                                                                                                                                                                                                                        LVEFTYFVLGFSAAIQDDNELIGQPEIQCNADTIDMQFRTRKQFNGKVYVKGSYNRPECR
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                                                                                                                                                                                                                                                                                                                                     384 AA;
                                                                                                                                                                                                                                                                                       Conservative
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-MFSQTVYVMDKENGDSTSAQAAEIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9851916;
                                                                                                                                                                                                                                                                                                                           43964 MW;
                                                                                                                                                                                                                                                                                     27.0%; Score 546.5; DB 5; 31.2%; Pred. No. 2.3e-44; tive 75; Mismatches 155;
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01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
753HlB.1 protein.
Y53HlB.1.
  Q9XVN2
Q9XVN2;
01-NOV-1999
01-NOV-1999
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Science 282:2012-2018(1998).
EMBL; AL132851; CAB60411.1;
InterPro; IPR001507; Endog11n/CD105.
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                       AILQGSHPSTVVCLNQSRIQIFFVLSFLMLTVVTVLTIFTVRRSMTA
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                                                                                                                                                                                                                                                         DNGFNRRSRRA--TLSNRTAVNWVHLADTMDLAANKITVFELEEKQNSEDKDEPPAHSHL
                                                                                                                                                                                                                                                                                                LRLLKKRSAEPENIIDVRTDINTLEISDD-----NQALPVDLRHRALLQHNGQPVI---L
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  (TrEMBLrel.
                                                               PRELIMINARY;
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Pred. No. 3.2e-43;
                                                               PRT;
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O93967; O94405;
01-FEB-1997 (TEMBLEGL 0
01-NOV-1998 (TIEMBLEGL 0
01-MAR 2002 (TIEMBLEGL 2
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                    ZK265.8 protein.
ZK265.8.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
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SMART; SM00241; ZP; 1
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Science 282:2012-2018(1998).
EMBL; Z81086; CAB03116.1; -.
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
NCBI_TaxID=6239;
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                                                                                                                  SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                             Submitted (OCT-1996)
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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Caenorhabditis.
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Pred. No. 1
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Best Local
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                                                                                                                                                                                                                    W01A8.3 protein. W01A8.3.
                                                                                                                                                                                                                                              Q23097;
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                           Eukaryota; Metazoa;
Rhabditidae; Peloder
                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                          Q23097
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SMART; SM00241; ZP; 1.
SEQUENCE 440 AA; 49299 MW; 0507A68B1AEEC70F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z81143; CAB03520.1; --
EMBL; Z75713; CAB03520.1; JOINED.
EMBL; Z75713; CAB00057.1; --
EMBL; Z81143; CAB00057.1; JOINED.
"Genome sequence of the nematode C.elegans: A platform investigating biology."; Science 282:2012-2018(1998).
                                                           SEQUENCE FROM N.A. MEDLINE-99069613;
                                                                                                    Submitted (APR-1996)
                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1996)
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                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              EEEEKAPSSRR---KTTPKP
                                                                                                                                                                                                                                                                                                                                                                                                          AAKPAAAAQLRLLKKRSAEP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                     QRAYAESSVFKFADKPGVWFFCQVQMCMKK-HGMCDGITPPSCGSMSRVISVGGEDNGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      M-AGQEAHVYKYADRSQLFYQCQISITIKEPNSEC---VRPQC---SEPQGFGAVKTGGA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGERVLHQWHCNDQ---MYGVLINNCYVTDGFGKKADVIDDKGCPIDPILITGIRYSSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCFYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEI-----LDGG-PTGQPVQFAI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKILIIAWTGWRVANAISIDNEIIGEPDIECLEDEIRIWVKTRKIFAGRIYAKGRAELED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDL 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYKDDFGNOKTRKPHFDLOFGACGMKSLRSVDPRGMYYGITVVVSFHPLFITKVDQAYHV
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                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                         Peloderinae;
                                                            PubMed=9851916;
                                                                                                                                                                       Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.6%; Score 477.5; DB 5; 33.4%; Pred. No. 1.3e-37; tive 66; Mismatches 122;
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                                                                                                    the EMBL/GenBank/DDBJ databases
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RESULT 16
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                                                                                                                                                                                                                                                                                                                 investigating biology.", Science 282:2012-2018(1998).
EMBL; Z49071; CAA88879.1; -.
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
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O22680;
O1-NOV-1996 (TrEMBLrel. 01,
O1-NOV-1996 (TrEMBLrel. 01,
O1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001507; SMART; SM00241; ZP; SEQUENCE 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; z71267; CAA95850.2; InterPro; IPR001507; Endo
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WVMPKCEYSVRRDGPTLTYANVGDIVFHVWEC---TPADMGMLVKKCFVTDGDGEDH
ARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQIEVSEI-TTAF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-----APSPFCVPRLLLPVLPLILITIVSLT 323
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                                                                                                                                PEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGR---QVAGISLPF-DSCNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVRPQC-----SEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EILNADGCALDKYLLNNLEYPTDLM-AGQEAHVYKYADRSQLFYQCQISITIKEPN--SE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLNPRGIFVTTTVVISFHPL-FVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQTQI 147
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                                                                              PKLECGSEGIRLHINPTGTFGGHVYVRGFFPQTVCHLNYCTRLTNRPIVMDLPFRGPCNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIALIAAVIITIS 378
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                                                                                                                                                                                         . Similarity
99; Conserv
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                                                                                                                                                                                                                                                                                           609 AA;
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38767 MW; B8DED6CCE4D308F3 CRC64;
                                                                                                                                                                                                                                                                                           1.
68882 MW;
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                                                                                                                                                                                         41;
                                                                                                                                                                                   ; Score 451; DB; Pred. No. 7.5e
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Last annotation updat
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Best Local S
Matches 96
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01-NOV-1996
01-OCT-2001
01-DEC-2001
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fulton L.;
"The sequence of C. e
Submitted (APR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology. The C Science 282:2012-2018(1998). [2]
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01-OCT-2001 (TYEMBLYE1. 18, Last sequence update)
01-DEC-2001 (TYEMBLYE1. 19, Last annotation updat
Hypothetical 81.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 731 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2001) to tl
EMBL; U23449; AAC24298.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
       241
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                                                                                                                                                           120
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  KYADRSQLFYQCQISI--TIKEPNSECVRPQC--
                                                                                                                                                                                     FYMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWT
                                                                                                                                                                                                                                                                                       GCRNDEGGRQVAGISLPFDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQC
                                                       CPSE---AYOMEVYNCDVVGGEEYSKKVIGENGCSEDIYIMPNLIYNENRTKAFVNSNAF
                                                                                                      CDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTD-LMAGQEAHVY
                                                                                                                                                      FYKEAEKAVGAEVSVSDPTPVQLEDESPQPVCSYTIHKESPNGPIAKFAQLGDVLYHVWE
                                                                                                                                                                                                                                                          GC----SFSNTANATFEFSKCDVMRQREANPKGMAYTATVVVQLHPLFTTKVDRAYKLRC
                                                                                                                                                                                                                                                                                                                                                                                                           IAFCTTLIALSYS----IPVDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQE
                                                                                                                                                                                                                                                                                                                                                              IDFLLLMLALFNSAQPIVEFDNHISDEPEVSCHSGFMSLKVNTEKSPPSHVFVKGHFRKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e nematode C. elegans: a platform for The C. elegans Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 432.5; I
Pred. No. 5.9e<sup>.</sup>
53; Mismatches
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ID 92157
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DT 01-MA
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018213
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Best Local
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Q21573;
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018213;
SEQUENCE
                                                                                                                                                        M28.1.
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EMbu,
InterPro; Len.
InterPro; SM00241; '
                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                           01-NOV-1996 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                            M28.1.protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kershaw J.K., Lennard
Submitted (SEP-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematu
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TremBLrel.
01-JAN-1998 (TremBLrel.
01-MAR-2002 (TremBLrel.
                           NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 VDNGVEGEPEIECGPTSITINFNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLP--
                                                                                                                                                                                                                                                                              DNHIVYFKCNIRITVKNPSGECPVNNCS-PNG
                                                                                                                                                                                                                                                                                                          DRSQLFYQCQISITIKEPNSECVRPQCSEPQG 275
                                                                                                                                                                                                                                                                                                                                           APSDVYCIQVYSCTAEDGGSDTVQVVDENGCTTDGELLSPIKYKEGSMRAAASSHAFKFV
                                                                                                                                                                                                                                                                                                                                                                          T-VDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLM-AGQEAHVYKYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNSDIIGEPKIRCAPTGITIMLETDSPFKGALFLRGSADKKSCKANFSAQPSQNISFEFG
                                                                                                                                                                                                                                                                                                                                                                                                        APQPRILSDEPKLPTCDYRVEVTGGKAVAGGIVTSSLSETASQIANVGDSVIHIWTCSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                         EITTAFQTQIVPMPVCRYEI-LDGGP-----TGQPVQFAIIGQPVYHKWTCDSE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDDCPSRRKRQIVAPRGMTMSSVLVVSYHGSIITHRDVAYQIDCFYREENSRVETMLSVN
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FROM
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                                                                                                                                                                                             PRELIMINARY;
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                                             Nematoda; Chromadorea; cinae; Caenorhabditis.
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                                                                                                                         Last sequence update)
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Last sequence up
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Pred. No. 1
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l.6e-31;
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                                                              Rhabditida; Rhabditoidea;
                                                                                                                             update)
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Best Local
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Q9TZE2;
01-MAY-2000 (TrEMBLrel. 13, Createa,
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
uvnothetical 53.3 kDa protein.
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                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Fulton R., Rohlfing T., Morris M.;
"The sequence of C. elegans cosmid W04C9.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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EMBL; 249911; CAA90131.2; -.
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                            NCBI_TaxID=6239
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                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium. Science 282:2012-2018(1998).
                                                                                                                                                  None;
                                                                                                                                                                                                                                                                                                                                     Q9TZE2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISLPEDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCFYMEADKTVSAQI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTLEI-----SDDNQALPVDLRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSCFVDDGNGDTVEILNADGCALDKYLLNNLEYPTDLMAGQ-EAHVYKYADRSQLFYQCQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVNMTDEQEINGTVEPPSCDYLISD - - QNGNSVQNSLVGELVRHQWVCKGGLTNKLKMLV
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                                                                                                                                                            PubMed-9851916;
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Pred. No. 3.4e-
56; Mismatches
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Matches 79
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                                                                                  Query Match
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096776;
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                                                                                                                  NON_TER
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                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-99339397; PubMed-10413052;

F. K., Hunter S.J., Tetley L., Pavia Nunes
                                                                                                         SEQUENCE
                                                                                                                                       EMBL; AJ012618;
                                                                                                                                                             the
                                                                                                                                                                                                                                              Onchocercidae; E
NCBI_TaxID=6280;
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                              Brugia pahangi.
                                                                                                                                                                                                                                                                                         Cut-1
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                                                                                                                                                                    "cut-1-like genes are present in the
and Brugia malayi and, as in other ne
                                          166 PVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                         177
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.. Biochem. Parasitol. 101:173-183(1999).
RI: AJ012618; CAA10075.1; -.
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97.0%;
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Last annotation updat
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Pred. No. 2.2e-27;
1; Mismatches 1
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5; Mismatches
                                                                                                         A446D3C2686C3353 CRC64;
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Best Local :
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O61816; 01-AUG-1998 (
01-AUG-1998 (
01-MAR-2002 (
Hypothetical
B0511.5.
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Q19304;
Q1-NOV-1996
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; U41264; AAA82426.1; -.
InterPro; IPB001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Caenorhabditis.
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Hypothetical 49.1 kDa protein.
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STRAIN-BRISTOL N2;
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Submitted (DEC-1995)
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"The sequence
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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8 (TrEMBLrel. 07, Las
2 (TrEMBLrel. 20, Las
al 25.2 kDa protein.
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20, Last annotation update)
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EMBL/GenBank/DDBJ
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
"Genome sequence of the nematode C. elinvestigating biology. The C. elegans Science 282:2012-2018(1998).
                                        None;
                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                           Q9BKQ4
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AF067608; AAC17653.1; -.
InterPro; IPR001507; Endoglin/CD105.
SMART; SM00241; ZP; 1.
                                                                                        NCBI_TaxID=6239;
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SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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The C. elegans Sequencing Consort
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cosmid B0511.";
EMBL/GenBank/DDBJ
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Pred. No. 1
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SMART; SM00327; VWA; 2.
SMART; SM00241; ZP; 1.
PROSITE; PS50234; VWFA; 2.
Hypothetical protein.
SEQUENCE 789 AA; 89078 MW;
                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematorhabditidae; Peloderinae; NCBI_TaxID=6239;
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
T21B10.6 protein.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AC091267; AAK31565.1; .
InterPro; IPR001507; Endog1in/CD105.
InterPro; IPR002035; VWF_A.
Pfam; PF00092; Vwa; 2.
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Science 282:2012-2018(1998).
EMBL; 268318; CAA92696.1; -.
                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
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                                                                                    "Genome sequence of the nematode C.elegans:
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  IPR001507; Endoglin/CD105
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EMBL/GenBank/DDBJ
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Best Local S
Matches 82
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Best Local S
Matches 81
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                                                                                                                                     "Genome sequence of the nematode C.elegans: investigating biology "; Science 282:2012-2018(1998).

EMBL; Z82073; CAB04922.1; ...
InterPro; IPR001507; Endogin/CD105.
PRINTS; PR01651; SEGGEXPORT.
SMART; SM00241; ZP; 1.
SMART; SM00241; ZP; 1.
SEQUENCE 344 AA; 38563 MW; D3D50114B7B48
                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2002 (TrEMBLrel. 21, W06D12.1 protein. W06D12.1.
                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Basham V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00241; ZP; SEQUENCE 366 AA;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                            Rhabditidae;
                                                                     151
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                                                                   PVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEIL
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                      NADGCALDKYLLNNLEY-PTDLMAGQEAHVYKYADRSQLFYQCQISITIKE-----
                                             PVCKYEVLMENAQGPPLSHATVGDLYYHKWSCDGNNKEMYCMTVHSCVVDDGQGFGQKLV
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81; Conservative
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                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                          Peloderinae;
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                                                                                          14.3%; Score 290.5; DB 5; 27.4%; Pred. No. 1.2e-19; tive 45; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                          Caenorhabditis
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; Pred. No. 7.7e-20;
53; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
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                                                                                                                                        D3D50114B7B4891A CRC64;
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Best Local S
Matches 97
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EMBL; AP099921; AAC68807.1;
InterPro; IPR001507; Emdoglin/CD105.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002965; VWF_A.
InterPro; IPR002035; VWF_A.
InterPro; IPR002015; VWF_A.
INTERPO092; VWA; 1.
PRINTS; PR0017; PRICHEXTENSN.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00241; ZP; 1.
SMART; SM00241; ZP; 1.
PROSITE; PS50234; VWFA; 1.
PROSITE; PS50234; VWFA; 140794 MW; 957819B9BC127CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Geisel C., Kramer J., Smith A.
"The sequence of C. elegans cc
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Q1-MAY-2000 (TIEMBLITEL 1
Q1-MAY-2000 (TIEMBLITEL 1
Q1-MAR-2002 (TIEMBLITEL 2
MQ1EL), 2 protein.
  1021
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Shabditidae: Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
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AIAETISLSTLPPTCTYSIRKEGPEGPIVSRAVVGQTVWHRWECDGTNDTNQAYGIQVHS
                            TTAFQTQIVPM-PVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCD--SETVDTFCAVVHS
                                                                                                                        VARTRSLNPRGIFVTTTVVISEHPLFVTKVDRAYRVQCFY--MEADKTVSAQIEV--SEI 139
                                                                                                                                                                                                DLECYGDGFKYQYNPPAGFRGYAYVKGYQDDARC-----KATASSSLPLNLFISNNECG
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                                                                                               VTQVKSSDPNGLNSSLVLHLLHDDELNTAEDRAYLLQCFIGAQNQDAVVSTNLNVVRSEL
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                                                                                                                                                                                                                                                                                                                         14.3%;
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cosmid M01E10.";
EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                  Score 289.5; DB 5;
Pred. No. 8.7e-19;
6; Mismatches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                    957819B9BC127CCE CRC64;
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Best Local S
Matches 100
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Q9U3W7;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00181; EGF; 5.

SMART; SM00241; ZP; 1.

PROSITE; PS01186; EGF 2; UNKNOWN 4.

SEQUENCE 809 AA; 87817 MW; 07FD2F0445FD487C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP460.
SP460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insepterygota; Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0029129; SP460.
InterPro; IPR000561; EGF-like.
InterPro; IPR001507; Endoglin/CD105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1999) to the EMBL/GenBank/DDBJ EMBL; AF214523; AAF24502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serano T.L., Pendleton J.D., Rubin G.M.; "A reverse genetic screen for genes involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1141
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 RHRALLQHN---
                                         GGYNAFGR--
                                                        SEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISDDNQALPVDL
                                                                                                            GCALDKYLLNNLEYPTD----LMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQC
                                                                                                                                                                                                   SFYLVIQKHPKLYTYKAQAYNIKCYYQTGEKNYTLGFNVSMLTTAGTIANTGPPPICQMR
                                                                                                                                                                                                                          TTTVVISFHPLEVTKVDRAYRVQCFYMEADKTVSAQIEVSEITTAFQ-TQIVPMPVCRYE
                                                                                                                                                                                                                                                                            NAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLP------FDSCNVARTRSLNPRGIFV
                                                                                                                                                                                                                                                                                                          AFCN---AVNHRAQCQCITGYTGNPDLHCNHTNFRTDFPRPDMVVSCLADGVQVEIHITE
                                                                                                                                                                                                                                                                                                                                    AFCTTLIALSYSIPVD--NGVEGEPEIECGPTSITINEN------TR
                                                                                          GCATDTSIFGNWEYNPDTNSLLASFNA--FKFPSSDNIRFQCNIRVCF----GRCQPVNC
                                                                                                                                                IITN--EGEEINSAEIGDNL--KLQVDVEPATIYGGFARSCIAKTMEDNVQNEYLVTDEN
                                                                                                                                                                                                                                                       PGFNGVLYVKGHSKDEECRRVV----NLAGETVPRTEIFRVHFGSCGMQAVKDV-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFVDDGNGDTVEILNADGCALDKYLLNNLEYPTD-LMAGQEAHYYKYADRSQLFYQCQIS
                                                                                                                                                                         ILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDTFCAVVHSCF---VDDGNGDTVEILNAD
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              12.0%; Score 244; DB 5;
23.7%; Pred. No. 1.2e-14;
ive 54; Mismatches 162
GQPV----ILAAVQ--NGICMSPFGFSMFMGLSIALIAAVII
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13,
20,
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Last sequence update)
Last annotation updat
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                                      -RRRS----IADNSTDATAIA---TNSGVEGQL
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                                       703
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RESULT
Q22724
ID Q22724
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AC Q2
DT 01
DT 01
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Best Local Similarity
                                                                                                                                                                                                  Q22724;
01-NOV-1996
01-OCT-2001
01-MAR-2002
T24C2.1 prot
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Q1-OCT-2000 (TrEMBLrel. 15, 0)
Q1-OCT-2000 (TrEMBLrel. 15, 0)
Q1-MAR-2002 (TrEMBLrel. 20, 0)
Q1-MAR-2002 (TremBLrel. 20, 0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
SEQUENCE
                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDITINE=20359254; PubMed=10899109;
YU R.Y., Nguyen C.Q., Hall D.H., Chow K.L.;
"Expression of ram-5 in the structural cell ray morphogenesis in Caenorhabditis elegans EMBO J. 19:3542-3555(2000).

EMBL; AF218866; AAF67103.1; C.C.C.EMBL; AF218866; AAF67103.1; C.C.C.EMBL;
                                                                                                                                                                                                                                                                                                                                                                        Q22724
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Rhabditidae; Peloder
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InterPro; IPR000531;
SMART; SM00241; ZP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 MEADKTVSAQIEVSEITTAFQTQIVPMPV-----CRYEILDGGPTGQPVQFAIIGQ
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711 AA;
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                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TONB_DEPENDENT_REC_1; UNKNOWN_1.; 80883 MW; 25F9F4A06FFE27E6 CRC64;
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O9W143; O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. A., Daviner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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Science 282:2012-2018(1998).
EMBL; Z68120; CAA92199.2; -.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR000531; TonB_boxC.
SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tacheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Best Local S
Matches 94
Q9GUH4
Q9GUH4;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                        EPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSAEPENI - - - IDVRTDINT
                                                                                                                                                                                                                                                                                                                                                                             GWGEQRLVGEDGCPMDNEIMGQFNYTQDRLAANVTFPAHKFPYT--TSVYYQCNVRLCAL
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CE 462 AA;
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  (TrEMBLrel. 16,
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                      DSDEDAVYKEK-----TLDDALCVSQRTFAIAIAIAGLILMLAVVA
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                                                                                                                                                                                                                                                                                                   -GKRPKRQAAAD-----SKEEDGLPATIEVFSGLYV
  Created)
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Pred. No. 1
                                         PRT;
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.3e-10;
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Fleischmann
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RESULT 33
Q9VZC5
ID Q9VZC
AC Q9VZC
AC Q9VZC
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-JT
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Best Local
                                                                                                                   01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                         CG15020
                                                                                          CG15020 protein.
                                                                                                                                                                                                                  Q9VZC5
                        Eukaryota;
                                                   Drosophila
                                                                                                                                                                                          Q9VZC5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001507; SMART; SM00241; ZP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL; AC084196; AAG23450.1; EMBL; AC084196; AAK29949.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Rhabditidae; Peloderinae; Caer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIVAFHPTLVTPSDRAFRAHCEFEDFKRKTEIGIENLIQEHELILGNFQ-----LPKISM
                                                                                                                                                                                                                                                                                                                                                                                                                             -----IYVNGRFRVEKQSSPQEA-RATSQTEFCMPDVIY--YLGLSTVVICYLITISTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HILPAGEESLTTKTQNFEANEQKVLNVGDPIMFEWKLEQEH-GIFGIQLERCSAESENGK
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melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata;
Neoptera; Endopterygota; Diptera
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                                                                                                                                                                                                                                                                                                                                                                               381
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                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32361 MW;
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  Endopterygota; Diptera;
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                                                                                                                   Created)
Last sequence update)
Last annotation updat
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Pred. No. 1
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Sequencing Consort
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.8e-08;
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                        Hexapoda; Insecta;
                                                                                                                     update)
  Brachycera;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A., E., Garg N. S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabrielian A., E., Garg N. S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Munt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Rahert E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Yinskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA King Z.-Y., Wang S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA King Z.-Y., Wang S., Shan M., Zhang G., Zhao Q., Zheng 
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Best Local S
Matches 72
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Pfam; PF00100; zona_pellucida;
SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0035543; CG15020. InterPro; IPR001507; Endoglin/CD105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003481; AAF47899.1;
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221
   243
                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 EIECGPTSITINFNTRNAFEGHVYVKG-LYDQEGCRNDEGGRQVAGISLPFDSCNVARTR
                                                                           DIVVNDCYAHNGANKRIQLIDQHGCPVDDKLISRFRGSWSDSGVYETQVYAYMK--TFRF
                                                                                                                                                       CAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLE-----
ADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGAAAKPAAAAQLRLLKKRSA
                                                                                                                                                                                                                                   GNPVVFTLSPPECYMEIQNGYGIGGPRVTG-PVR---VGDPLTLIIYMR-----SKYDGF
                                                                                                                                                                                                                                                                                                               AFQTQI-VPMPVCRYEILD----GGP--TGQPVQFAIIGQP----VYHKWTCDSETVDTF
                                                                                                                                                                                                                                                                                                                                                                                   SLQEESRKNPTN-FMWNTVTVQYNPLIEEEYDEHFKVTCEYGYDFWKTVTFPFLDVEVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAECQDDYMKIRIGFNGSFSGLLYSAGYAYDPDCMYINGSGRDYYEFYIQLNRCGTLGKN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SL-----NPRGIFYTTTVVISFHPLFVTKVDRAYRVQCFY-MEADKTVSAQIEVSEITT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.2%; Score 166; DB 5; 22.0%; Pred. No. 2.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2AB0F245A01DC46B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 604;
                                                                                                                                                       -YPTDLMAGQEAHVYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                               448
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Best Local
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FlyBase; FBgn0016047; nompA.
InterPro; IPR001604; Crystallin.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR003014; PAN.
InterPro; IPR003019; Pan_app.
Pfam; PF00024; PAN; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00473; PAN_AP; 4.

SMART; SM00241; ZP; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

Receptor; Signal.

SIGNAL

1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insu
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21134724; PubMed=11239432; Chung Y.D., Zhu J., Han Y., Kernan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No-mechanoreceptor potential A short isoform precursor NOMPA OR CG13207.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BMD4
1326 QLGEKTKETEEPEQVREMIEVFETREEIEKESYPRKLVAPVETVCMTP---AEYHGLITA 1382
                                                                                                                                                                                                                                             1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                            168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYPDCGTQR-----YGDTLTNIVVVQFSDNVQTSRDKRYNLTCIFRGPGEAVVSSGYIG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRSDGECMDVTQTCNEEGMEFTIRTPEGFLGRIYTYGFYDRCFFRGNGGTYNVLRLSGPQ 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEPEIECGPTSITIN-----FNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLP- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTSNM--TATNISIPPLSADGEGLTTE
                                                                                                                                                                              AAKPAAAAQLRLLKKRS-AEPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                     QFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----YMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPT-----GQPV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -FDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCF------ 122
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                                                                                                                      RQEPSFGRRRSLNTTEIPEPEALALEGSSQLEASTLDEVTVVNSTTVSATLGQVPLNET
                                                                                                                                                                                                                                          LRDGDTLEA--RFNAFKIPESNFLVFEA----TVRSCREGCQPAYCPGPAG-----
                                                                                                                                                                                                                                                                                                  PTD---LMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGA 284
                                                                                                                                                                                                                                                                                                                                                                TFRLEAQDGYNHVT-----DIFATNVVA--RDPYSGRSIQLIDRFGCPVDPFVFPELDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1549 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 POTENTIAL.
174271 MW; 78C31E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%;
                                                        ----LRHRALLQHNGQPVILAAVQNGICMSPFGFSMFMGLSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163; DB 5; Length 1549; Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78C31BACA39D5B93 CRC64;
                                                                                                                                                                              ----NIIDVRTDINTLEISDDNQALPVD--
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Q9BMD5
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InterPro; IPR001064; Crystallin.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chung Y.D., Zhu J., Han Y., Kernan M.J.;
"nompA encodes a PNS-specific, ZP domain protein required to connect mechanosensory dendrites to sensory structures.";
Neuron 29:415-428(2001).
EMBL, AF334031; AAK09433.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NO-mechanoreceptor potential A long isoform precursor.
NOMPA OR CG13207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00024; PAN; 5.
SMART; SM00473; PAN_AP; 4.
SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BMD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21134724; PubMed=11239432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                27
QLGEKTKETEEPEQVREMIEVFETREEIEKESYPRKLVAPVETVCMTP---AEYHGLITA
                                                                                                                                           PTD---LMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGA
                                                                                                                                                                                    TFRLEAQDGYNHVT-----DIFATNVVA--RDPYSGRSIQLIDRFGCPVDPFVFPELDK
                                                                                                                                                                                                           QFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEY
                                                                                                                                                                                                                                                                                                                 GYPDCGTQR-----YGDTLTNIVVVQFSDNVQTSRDKRYNLTCIFRGPGEAVVSSGYIG
                                                                                                                                                                                                                                                                                                                                                  -FDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCF---------
                                                                                                                                                                                                                                                                                                                                                                              GRSDGECMDVTQTCNEEGMEFTIRTPEGFLGRIYTYGFYDRCFFRGNGGTVNVLRLSGPQ 1072
                                                                                                                                                                                                                                                                                                                                                                                                             GEPEIECGPTSITIN-----FNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLP- 78
                           RQEPSFGRRRRSLNTTEIPEPEALALEGSSQLEASTLDEVTVVNSTTVSATLGQVPLNET
                                                                                        AAKPAAAAQLRLLKKRS-AEPE------NIIDVRTDINTLEISDDNQALPVD--
                                                                                                                         LRDGDTLEA--RFNAFKIPESNFLVFEA----TVRSCREGCQPAYCPGPAG------
                                                                                                                                                                                                                                                    AGSGSPIPIEYLPAENTLSSKVRLS--------ILYQGRPTTTIAVGDPL
                                                                                                                                                                                                                                                                                   ----YMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPT-----GQPV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1557 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 POT
175291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 163; DB 5
Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134BBBBA89245183 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1557 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB_5; Length 1557;
                                                                                                                                                                                                                                                                                                                                                                                                                                           155; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                           1325
                                                                                                                                                                                                                                                                                                                   1126
                                                                                          329
                                                                                                                                                                                       1220
                                                                                                                                                                                                                                                    1168
                                                                                                                                                                                                                     227
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PRESULT OPENITATION OF THE CONTROL O
                                                                                                                                                                                                                                                                                                                                RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L., Beasley E.M.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchen A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guna P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guna P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guna P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., My M., Murphy B., Murphy L., Murny D.M., Nelson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Pittman G.S., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Pittman G.S., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Walson S.I., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Stapleton M., Stupski M.P., Smith T.,
RA Palazzolo M., Stapleton M., Stupski M.P., Smith T.,
RA Palazz
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                                                                                                                                                              FlyBase; FBgn0016047; nompA.
InterPro; IFR001064; Crystallin.
InterPro; IFR001507; Endoglin/CD105
InterPro; IFR003011; PAN.
InterPro; IFR003609; Pan_app.
                                                                                                                                                Pfam;
SMART; SM00473; PAN_AP; 4.

SMART; SM00241; ZP; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1

SEQUENCE 1638 AA; 184367 MW; 791620EABFA3EB15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro
NCBI_TaxID=7227;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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01-MAR-2002
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V5X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1383 IILLMILLFS 1392
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                                                                                                                                            PF00024; PAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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   791620EABFA3EB15 CRC64;
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RX MEDILINE-20196006; PubMed-10731132;

RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Barlew R.M., Baybayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Charles S.M., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,

RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VZEO;
01-MAY-2000
01-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CG15013 protein. CG15013.
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                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VZE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1174 AGSGSPIPIEYLPAENTLSSKVRLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GEPEIECGPTSITIN-----FNTRNAFEGHVYVKGLYDQEGCRNDEGGRQVAGISLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IILLMILLES 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIAAVIITIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQEPSFGRRRRSLNTTEIPEPEALALEGSSQLEASTLDEVTVVNSTTVSATLGQVPLNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRDGDTLEA--RFNAFKIPESNFLVFEA----TVRSCREGCQPAYCPGPAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFAIIGQPVYHKWTCDSETVDTFCAVVHSCFVDDGNGDTVEILNADGCALDKYLLNNLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YMEADKTVSAQIEVSEITTAFQTQIVPMPVCRYEILDGGPT-----GQPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYPDCGTQR-----YGDTLTNIVVVQFSDNVQTSRDKRYNLTCIFRGPGEAVVSSGYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRSDGECMDVTQTCNEEGMEFTIRTPEGFLGRIYTYGFYDRCFFRGNGGTVNVLRLSGPQ 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAKPAAAAQLRLLKKRS-AEPE------NIIDVRTDINTLEISDDNQALPVD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTD----LMAGQEAHVYKYADRSQLFYQCQISITIKEPNSECVRPQCSEPQGFGAVKTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -FDSCNVARTRSLNPRGIFVTTTVVISFHPLFVTKVDRAYRVQCF--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85;
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O (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%;
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A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Syirskas R., Moodage T., Weinstock G.M., Weissenbach J.,
A Sylins S.M., Woodage T., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
BE EMBL; ABG09480; AAF47884.1; -
BREL; ABG09480; AAF47884.1; -
BREL; SMADY SMADON SMAD
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2 T21H3.4 protein.
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Cou Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnst Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                    STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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51; Mismatches
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                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                            SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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  Adams M.D., Celn
Amanatides P.G.,
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EMBL; AFO16429; AAB65365.1; -
INTERPROJEMBL; EMOGILIN/CD105.
SMART; SM00241; ZP; 1
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67; Conserv
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  Celniker S.E.,
P.G., Scherer S.
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20,
  Holt
E., I
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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  t R.A., Evans C.A.,
Li P.W., Hoskins R.
                                                                                                                                                                                                                                                                                                                                                                                                                                          758
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                                                                                                                                                                                                          Brachycera; Muscomorpha;
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  R.F.
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harli J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ra Ballew R.M., Basu A., Baxendale J., Bayrattaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evanqelista C.G., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitaky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Muzphy L., Muzny D.M., Welson D.L.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Sunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y. Wassarman D.A., Welfstock G.M., Welssenbach J.,
RA Wang Z.-Y. Massarman D.A., Welfstock G.M., Welssenbach J.,
RA Harlinas S.M., Wood M., Strong R., Sun S.,
Ra Lenguard C.D., Krabits C.C., Wu D., Yang S., Yao Q.A.,
RA Harli M., Sheng S., Pan S., Pan S., Pan M., Zhang G., Zhao Q., Zheng Y., Pan M., Zhang G., Zhao Q., Zheng Y., Welssenbach J.,
Ra Harli M., Welson M., Welson M., Welson D., Welson M., Wel
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Best Local
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SMART; SM00473; PAN_AP; 3.
SMART; SM00241; ZP; 1.
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 651
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                                     --TGGAAAKPAAAAQLRLLKKRSAEPENIIDVRTDINTLEISD
                                                                                                                                                                                                                             GEIESTLSEEIIVDSPNVIMKITARDG---SDMKRIAEVGDPLALRF----EIVDANSPY
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NGTDGVELAIKSERQKRDVSHQAAGDENILLVQ---
                                                                                                             LFYQCQISITIKEPNSECVR-----
                                                                                                                                                     EIFVRELVAMDGT-DSAEITLIDANGCPTDQYIMSAMQ---
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                                                                           LLSQFD---AFKFPSSELVQFRALVTPCIPRC-EPVICDNDENGELKSLLSYGRRKRSVL
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                                                                                                           -PQCSEP----
 SIQITD
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 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY051820; AAK93244.1;

FlyBase; FBgn0039851; CG12063.

SEQUENCE 362 AA; 39728 MW; FC23553EAOD431CE CRC64;
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CG12063.
CG12063.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0960V7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                           331 RHRALLQHNGQPVILAAVQNGICMSPEGF----SMEMGLSIALIA 371
                                                                                                                                                     265 RQKRDVSHQAAGDENILLVQ----SIQITDKFAFNGADAPGGSGSEAGGLDGLAKLQLDL
                                                                                                                                                                            164 -DSAEITLIDANGCPTDQYIMSAMQ------KLANNRKVLLSQFD---AFKF
                                                                                                                                                                                                                                                                                                                                 204 GDTVEI--LNADGCALDKYLLNNLEYPTDLMAGQEAHVYKYA-DRSQLFYQCQISITIKE 260
                                                                                                                                                                                                                                                                                                                                                                                        111 DSPNVIMKITARDG---SDMKRIAEVGDPLALRF----EIVDANSPYEIFVRELVAMDGT 163
                                                                                                                                                                                                                                                                                                                                                                                                              149 --PMPVCRYEILDGGPTGQPVQFAIIGQPVYHKWTCDSETVDT---FCAVVHSCFVDDGN 203
                                                                                                                                                                                                                                                                       261 PNSECVR------PQCSEP-----QGFGAVK-----TGGAAAKPAAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 RGIFVTTTVVISEHPLFVTKVDRAYRVQCFYMEADKTVSAQIEV---SEITTAFQTQIV- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TSKLFDGKVYAKGA--PKSCAVNVNN-----SLEFDLKMRYNDLECNVRQSAYGRYMN-
                                                                                                                                                                                                                              PSSELVQFRALVTPCIPRC-EPVICDNDENGELKSLLSYGRRKRSVLNGTDGVELAIKSE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DIVIOHHDMIVTSSDLGLAVSCQYDLTNKTVVNNVDLGVTGEIESTLSEEIIV 110
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                                                                          -----GTKSDTCINGYGFIIAGALFLLLQLTVIA 349
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